

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 07:17:45 ; Search time 1411 Seconds
(without alignments)
15357.591 Million cell updates/sec

Title: US-10-067-977-1
Perfect score: 1338
Sequence: 1 atgggggagatgcagggcgc.....ccacggactcttctctctga 1338

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estc:*
9: gb_est1:*
10: gb_est2:*
11: gb_estc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
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21: em_gss_vrt:*
22: em_gss_fun:*
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24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	809.8	60.5	895	14	BQ925372
2	808.4	60.4	1072	13	BM455819
3	795.8	59.5	887	13	BI259163
4	771	57.6	1006	13	BM542149
5	757.2	56.6	888	14	BQ425968
6	751.6	56.2	938	14	BQ936977

7	746.4	55.8	992	14	BQ934765	BQ934765
8	730.2	54.6	851	13	BI764996	BI764996
9	712.8	53.3	741	9	AUI134278	AUI134278
10	709.8	53.0	736	12	BG575325	BG575325
11	707.4	52.9	811	9	AL530006	AL530006
12	707	52.8	969	13	BI333256	BI333256
13	702.6	52.5	1070	13	BM460788	BM460788
14	701	52.4	940	14	BQ714990	BQ714990
15	698.4	52.2	845	12	BG762418	BG762418
16	697.8	52.2	849	14	BQ428408	BQ428408
17	695	51.9	1033	14	BQ051239	BQ051239
18	684.8	51.2	910	13	BI256003	BI256003
19	675.2	50.2	923	13	BI551358	BI551358
20	671.6	50.2	799	9	AU080100	AU080100
21	664.4	49.7	827	9	AUI121914	AUI121914
22	651.8	48.7	860	9	AUI18064	AUI18064
23	639.6	47.8	786	12	BE901422	BE901422
24	630	47.1	933	14	BQ888361	BQ888361
25	621.4	46.4	668	10	BE304666	BE304666
26	621	46.4	898	14	BQ687393	BQ687393
27	620.4	46.4	909	13	BM006359	BM006359
28	620.2	46.4	860	12	BF689365	BF689365
29	620	46.3	997	14	BQ691213	BQ691213
30	617.4	46.1	835	13	BI657111	BI657111
31	616.2	46.1	873	13	BI651188	BI651188
32	611.8	45.7	782	9	AUI135766	AUI135766
33	607.4	45.4	953	13	BI851305	BI851305
34	602.8	45.1	915	14	BQ959701	BQ959701
35	601.6	45.0	700	10	BE547715	BE547715
36	601.2	44.9	908	13	BM015162	BM015162
37	601	44.9	758	13	BI838931	BI838931
38	598.8	44.8	735	9	AL598724	AL598724
39	597	44.6	765	12	BG763506	BG763506
40	595.2	44.5	906	12	BG715428	BG715428
41	594.2	44.4	713	9	AUI136345	AUI136345
42	589	44.0	802	12	BG706343	BG706343
43	587.4	43.9	846	13	BI458251	BI458251
44	586.6	43.8	795	9	AUI140023	AUI140023
45	584.6	43.7	825	13	BI670405	BI670405

ALIGNMENTS

RESULT 1
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LOCUS BQ925372 895 bp mRNA linear EST 20-AUG-2002
DEFINITION AGENCOURT_8732778 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6455661
5', mRNA sequence.
ACCESSION BQ925372
VERSION BQ925372.1 GI:22340403
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 895)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC2634 row: k column: 22
High quality sequence stop: 685.
Location/Qualifiers
source 1. .895

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/clone="IMAGE:6455661"
/clone_lib="NIH_MGC_101"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT: 235 a 233 c 215 g 211 t 1 others
ORIGIN

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Query Match 60.5%; Score 809.8; DB 14; Length 895;
Best Local Similarity 97.5%; Pred. No. 1.3e-218;
Matches 844; Conservative 0; Mismatches 18; Indels 4; Gaps 2;

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QY 1 ATGGGGAGATGCGGGCGGCTGGCCAGAGCCGGCTCGAGTCCCTGCTGGCGGCCCGC 60
DB 15 ATGGGGAGATGCGGGCGGCTGGCCAGAGCCGGCTCGAGTCCCTGCTGGCGGCCCGC 74
QY 61 CACAAAAGAGGCGGAGGCGCAGAAAAGAGGAGGAGTCTTCTGCTGAGCGACTGGCT 120
DB 75 CACAAAAGAGGCGGAGGCGCAGAAAAGAGGAGGAGTCTTCTGCTGAGCGACTGGCT 134
QY 121 TTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTATTTCAGAGAGTTGCCAATACTC 180
DB 135 TTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTATTTCAGAGAGTTGCCAATACTC 194
QY 181 TATGCATGCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCACTCAGGAGCCT 240
DB 195 TATGCATGCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCACTCAGGAGCCT 254
QY 241 GAGCTTATGAATGCAACCCCTTCTCCTCCACCAAGTCTTCTCAGCAAAATCAACCTTGGC 300
DB 255 GAGCTTATGAATGCAACCCCTTCTCCTCCACCAAGTCTTCTCAGCAAAATCAACCTTGGC 314
QY 301 CCGTCGTCCTCAATCTCTAATCAACCATCTGACTTTCACTTTCTTGAAGATGATCGGAAG 360
DB 315 CCGTCGTCCTCAATCTCTAATCAACCATCTGACTTTCACTTTCTTGAAGATGATCGGAAG 374
QY 361 GGCAGTTTTGGAAGGTTCTTCTAGCAAGACACAGGCGAGAGTGTCTTATGCAATC 420
DB 375 GGCAGTTTTGGAAGGTTCTTCTAGCAAGACACAGGCGAGAGTGTCTTATGCAATC 434
QY 421 AAAGTTTTACAGAGAAAGCAATCTCGAAAGAAAGAGGAGGAGCATATATTATGTCGGAG 480
DB 435 AAAGTTTTACAGAGAAAGCAATCTCGAAAGAAAGAGGAGGAGCATATATTATGTCGGAG 494
QY 481 CGGAATGTTCTGTTGAAGATGTGAAGCACCCTTTCTCGTGGGCCCTTCACTTCTCTTC 540
DB 495 CGGAATGTTCTGTTGAAGATGTGAAGCACCCTTTCTCGTGGGCCCTTCACTTCTCTTC 554
QY 541 CAGACTCTGACAAATTTGTAATTTGCTCTAGACTACATTAATGCTGAGAGTGTCTTCTAC 600
DB 555 CAGACTCTGACAAATTTGTAATTTGCTCTAGACTACATTAATGCTGAGAGTGTCTTCTAC 614
QY 601 CATCTCCAGAGGAAAGCCTGCTTCTCGAAGAACCCGGGCTGTTTCTATGCTGCTGAATA 660
DB 615 CATCTCCAGAGGAAAGCCTGCTTCTCGAAGAACCCGGGCTGTTTCTATGCTGCTGAATA 674
QY 661 GCCAGTGCCTTGGGCTACCTGCAATCTAGCAATCGTTTATAGAGACTTAAACACAGAG 720
DB 675 GCCAGTGCCTTGGGCTACCTGCAATCTAGCAATCGTTTATAGAGACTTAAACACAGAG 734
QY 721 AATATTTGTAGATTACAGGGGACACATTTGCTTACTGACTCTCGAGCTCTCGAAGGAG 780
DB 735 AATATTTGTAGATTACAGGGGACACATTTGCTTACTGACTCTCGAGCTCTCGAAGGAG 794

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QY 781 AACATTGAACACACAGCAGCAATCCACCTT-CTGTGGCAGCC---GGAGTATCTCGC 836
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QY 837 ACTGAGGTGCTTCATAGCAGCCTT 862
DB 855 CCGGAGTGCCTTCAAGCAGCCTT 880

RESULT 2
BM455819 1072 bp mRNA linear EST 05-FEB-2002
LOCUS AGENCOURT 6409166 NIH_MGC 85 Homo sapiens cDNA clone IMAGE:5498261
DEFINITION 5', mRNA sequence.
ACCESSION BM455819
VERSION BM455819.1 GI:18504859
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1072)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLAM12129 row: 1 column: 06
High quality sequence stop: 640.

FEATURES
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1..1072
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5498261"
/clone_lib="NIH_MGC 85"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lymph: Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."
BASE COUNT 282 a 277 c 250 g 262 t 1 others
ORIGIN

Query Match 60.4%; Score 808.4; DB 13; Length 1072;
Best Local Similarity 94.4%; Pred. No. 3.6e-218;
Matches 903; Conservative 0; Mismatches 47; Indels 7; Gaps 6;

QY 116 TGCTTTTCATGAGCAGAGGAGTGGTCTGAACACCTTTATTTCAGAGATTGCCAATA 175
DB 118 TGCTTTTCATGAGCAGAGGAGTGGTCTGAACACCTTTATTTCAGAGATTGCCAATA 177
QY 176 ACTCTTATGATGCAACACCCCTTCAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235
DB 178 ACTCTTATGATGCAACACCCCTTGAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 237
QY 236 AGCTGAGCTTATGAATGCAACCCCTTCTCTCCACCAAGTCTCTTCAGCAATCAACC 295
DB 238 AGCTGAGCTTATGAATGCAACCCCTTCTCTCCACCAAGTCTCTTCAGCAATCAACC 297
QY 296 TTGGCCCGCTCGTCCCAATCTCATGCTAAACCATCTGACTTTCTTCTTGAAGTGTATCG 355
DB 298 TTGGCCCGCTCGTCCCAATCTCATGCTAAACCATCTGACTTTCTTCTTGAAGTGTATCG 357
QY 356 GAAAGGGCAGTTTTTGGAAAGGTTTCTTCTAGCAGACACAGGCAAGAGTGTCTTCTATG 415

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Db 358 GAAAGGCGAGTTTGGAAAGGTTCTTCTGCAAGACACAAGGAGGAGAGTGTCTATG 417
Qy 416 CAGTCAAAGTTTACAGAGAAAGCAATCTCTGAAAGAAAGAGGAGGAGCATATATGT 475
Db 418 CAGTCAAAGTTTACAGAGAAAGCAATCTCTGAAAGAAAGAGGAGGAGCATATATGT 477
Qy 476 CGAGCGGAATGTTCTGTTGAAGAAATGGAAGACACCTTTCTGTTGGGGCTTCACCTCT 535
Db 478 CGAGCGGAATGTTCTGTTGAAGAAATGGAAGACACCTTTCTGTTGGGGCTTCACCTCT 537
Qy 536 CTTTCCAGACTGCTGACAAATGTTGTTCTGTTGTTCTGTTGTTCTGTTGTTCTGTTGTT 595
Db 538 CTTTCCAGACTGCTGACAAATGTTGTTCTGTTGTTCTGTTGTTCTGTTGTTCTGTTGTT 597
Qy 596 TCTACCAATCTCCAGAGGAAAGCGTCTTCTGTTGTTCTGTTGTTCTGTTGTTCTGTTGTT 655
Db 598 TCTACCAATCTCCAGAGGAAAGCGTCTTCTGTTGTTCTGTTGTTCTGTTGTTCTGTTGTT 656
Qy 656 AAATAGCAGTGGCTTGGGCTACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 715
Db 657 AAATAGCAGTGGCTTGGGCTACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 716
Qy 716 CAGAGATATTTGCTAGATTTCAGAGGACACATTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 774
Db 717 CAGAGATATTTGCTAGATTTCAGAGGACACATTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 776
Qy 775 AAGGAGAAATTTGAAACACAGACACATCTCCACCTTTCTGTTGTTGTTGTTGTTGTTGTTGTT 833
Db 777 AAGGAGAACTTGNAC-CACAGACACACATCTCCACCTTTCTGTTGTTGTTGTTGTTGTTGTTGTT 835
Qy 834 CGACCTGAGTGGCTTCAAGAGCCTTATGACAGACTGTTGAGACTGTTGAGCTGTTGAGCTGTT 893
Db 836 CGACCTGAGTGGCTTCAAGAGCCTTATGACAGACTGTTGAGACTGTTGAGCTGTTGAGCTGTT 895
Qy 894 AGCTGCTTGTATGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 953
Db 896 AACTGCTTGGATGAAAGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
Qy 954 AATGTAGCAGCAATCTTGAACAGCCTCTCCAGCTGAAACCAAAATATACAAATTTCCCGC 1013
Db 955 AATGTCCGACACTTCCGACAGCTCTTCCAGCTGAAACCAATATACAAATTTCCCGC 1014
Qy 1014 AAGACACTCTGAGGGCTCTC--TCGAGAGGACAGGACAAAGCGCTTCGGGGC 1068
Db 1015 CAGAAACCTCCGAGGCCCCCTCGCAAAAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1071

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RESULT 3

B1259163
 LOCUS 602970006F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109625 5',
 DEFINITION mRNA sequence.

ACCESSION B1259163
 VERSION B1259163.1 GI:14816226
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 887)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LLAM1265 row: k column: 02
 High quality sequence stop: 790.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:5109625"
 /issue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."

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ORIGIN				
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Best Local Similarity	98.1%	Pred. No. 1.2e-214		
Matches	858	Conservative 0	Mismatches 12	Indels 5
Gaps	5			
Qy	375	GGTTCTTCTAGCAAGACACAAAGCAGAA-GAAGTGTCTATGCAAGTCAAGTCTTACAGA	433	
Db	13	GGTTCTTCTAGCAAGACACAAAGCAGAAAGTGTCTATGCAAGTCAAGTCTTACAGA	72	
Qy	434	AGAAACAATCTCTGAAAAAGAAAGAGGAGGAGCATATTTATGTCGGAGCGGAATGTTCTGT	493	
Db	73	AGAAACAATCTCTGAAAAAGAAAGAGGAGGAGCATATTTATGTCGGAGCGGAATGTTCTGT	132	
Qy	494	TGAGAGTGTGAGGACACCTTCTGTTGGGCTTCCACCTTCTTCTTCCAGACTGCTGACA	553	
Db	133	TGAAGAAATGTAAGACACCTTCTGTTGGGCTTCCACCTTCTTCTTCCAGACTGCTGACA	192	
Qy	554	AATTGTACTTGTCTCTAGACTACATTAATGTTGGAGAGTGTCTACCACTCTCCAGAGG	613	
Db	193	AATTGTACTTGTCTCTAGACTACATTAATGTTGGAGAGTGTCTACCACTCTCCAGAGG	252	
Qy	614	AACGCTGCTTCTGGAACCAACCGGCTCGTTTCTATGCTGCTGAAATGACGAGTGTCTGG	673	
Db	253	AACGCTGCTTCTGGAACCAACCGGCTCGTTTCTATGCTGCTGAAATGACGAGTGTCTGG	312	
Qy	674	GCTACTGCTATTCACCTGAAACATGTTTATAGAGACTTAAACCAGAGAGATATTTCTGCTAG	733	
Db	313	GCTACTGCTATTCACCTGAAACATGTTTATAGAGACTTAAACCAGAGAGATATTTCTGCTAG	372	
Qy	734	ATTCACAGGACACATTTGCTTACTGACTTCGGACTCTGCAAGAGAGACATTTGAACACA	793	
Db	373	ATTCACAGGACACATTTGCTTACTGACTTCGGACTCTGCAAGAGAGACATTTGAACACA	432	
Qy	794	ACAGCACACATCCACCTTCTGTGGCACCGGAGTATCTCGACCTGAGGTGCTTCAATA	853	
Db	433	ACAGCACACATCCACCTTCTGTGGCACCGGAGTATCTCGACCTGAGGTGCTTCAATA	492	
Qy	854	AGCAGCTTATGACAGGACTGAGACTGTTGTTGGCTCGGAGCTGTTGTATGAGATGC	913	
Db	493	AGCAGCTTATGACAGGACTGAGACTGTTGTTGGCTCGGAGCTGTTGTATGAGATGC	552	
Qy	914	TGTATGCTGCTGCGCTTTTATAGCCGAAACACAGCTGAAATGTACGACCAACATTTCTGA	973	
Db	553	TGTATGCTGCTGCGCTTTTATAGCCGAAACACAGCTGAAATGTACGACCAACATTTCTGA	612	
Qy	974	ACAAGCTCTTCCAGCTGAAACCAATATTTACAAATTTCCGACAGACACCTCTCGGAGGCC	1033	
Db	613	ACAAGCTCTTCCAGCTGAAACCAATATTTACAAATTTCCGACAGACACCTCTCGGAGGCC	672	
Qy	1034	TCCTGAGAGGACAGGACAAAGCGCTCGGGCCCAAGATGACTTCAATGAGATTAAGA	1093	
Db	673	TCCTGAGAGGACAGGACAAAGCGCTCGGGCCCAAGATGACTTCAATGAGATTAAGA	732	
Qy	1094	GTCACTGCTTCTTCTTAAATTAATCT-GGGATGATCTCAATTA-TAAGAAGATTAATCTCC	1151	
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Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT 235 a 218 c 207 g 227 t 1 others
ORIGIN
Query Match 56.6%; Score 757.2; DB 14; Length 888;
Best Local Similarity 99.6%; Pred. No. 1.1e-203;
Matches 759; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 63 TCGCTTTCATGACAGGAGGATGGTCTGAACGACTTATTTCAGAGATTGCCAATA 122
Qy 176 ACTCTATGATGCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCACTCAGG 235
Db 123 ACTCTATGATGCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCACTCAGG 182
Qy 236 AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTTTCAGCAATCAACC 295
Db 183 AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTTTCAGCAATCAACC 242
Qy 296 TTGGCCCGTCTGCTCAATCCTCATGCTAAACCATCTGACTTTCACCTTTGAAAGTATCG 355
Db 243 TTGGCCCGTCTGCTCAATCCTCATGCTAAACCATCTGACTTTCACCTTTGAAAGTATCG 302
Qy 356 GAAAGGCGAGTTTGGAAAGGTTCTCTAGCAACACCAAGGAGAGAGAGTGTCTATG 415
Db 303 GAAAGGCGAGTTTGGAAAGGTTCTCTAGCAACACCAAGGAGAGAGAGTGTCTATG 362
Qy 416 CAGTCAAAAGTTTACAGAGAAAGCAATCTCTGAAAAAGAGAGAGAGCAATATATGT 475
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Qy 476 CGAGCGGAATGTTCTGTTGAAGATGTGAAGCAACCCCTTCTGGTGGGCTTCACCTCT 535
Db 423 CGAGCGGAATGTTCTGTTGAAGATGTGAAGCAACCCCTTCTGGTGGGCTTCACCTCT 482
Qy 536 CTTTCCAGACTGCTGACAAATGACATTTGCTCTAGACTACATTAATGGTGGAGATGT 595
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Qy 836 CACTGAGGTGCTTTCATAAGCAGGCTTATGACAGGACTGTGG 877
Db 783 CACTGAGGTGCTTTCATAAGCAGGCTTATGACAGGACTGTGG 824
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BQ936977 938 bp mRNA linear EST 21-AUG-2002
LOCUS AGENCOURT 10056510 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6480313
DEFINITION 5', mRNA sequence.
ACCESSION BQ936977
VERSION BQ936977.1 GI:22352360
KEYWORDS EST.
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human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 938)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LCM2659 row: 0 column: 02
High quality sequence stop: 656.
FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
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/notes="Organ: prostate; Vector: pOTB7; Site: 1: XhoI;
Site: 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
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Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 238 a 255 c 227 g 217 t 1 others
ORIGIN
Query Match 56.2%; Score 751.6; DB 14; Length 938;
Best Local Similarity 98.2%; Pred. No. 4.6e-202;
Matches 803; Conservative 0; Mismatches 9; Indels 6; Gaps 4;
Qy 1 ATGGGGAGATG CAGGGCGCTGGCCAGAGCCGCTCGAGTCCCTGCTGCGGCCCGCC 60
Db 60 ATGGGGAGATG CAGGGCGCTGGCCAGAGCCGCTCGAGTCCCTGCTGCGGCCCGCC 119
Qy 61 CACAAAAGAGGCCCGAGGCGGAGAAAGAGGAGGAGTCTTCTGCTGAGCGGACTGGCT 120
Db 120 CACAAAAGAGGCCCGAGGCGGAGAAAGAGGAGGAGTCTTCTGCTGAGCGGACTGGCT 179
Qy 121 TTCTATGAGCAGAGGAGGATGGGTCTGAACGACTTTATTTCAGAAAGATTGCCAATACTCC 180
Db 180 TTCTATGAGCAGAGGAGGATGGGTCTGAACGACTTTATTTCAGAAAGATTGCCAATACTCC 239
Qy 181 TATGCAATGCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGGAGCCT 240
Db 240 TATGCAATGCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGGAGCCT 299
Qy 241 GAGCTTATGATGCCAACCCCTTCTCTCCACCAAGTCTTCTCAGCAAAATCAACCTTGGC 300
Db 300 GAGCTTATGATGCCAACCCCTTCTCTCCACCAAGTCTTCTCAGCAAAATCAACCTTGGC 359
Qy 301 CCGTCTGCAATCTCATGCTAAACCATCTGACTTTTCACTTTCTTGAAGATGATCGGAAG 360
Db 360 CCGTCTGCAATCTCATGCTAAACCATCTGACTTTTCACTTTCTTGAAGATGATCGGAAG 419
Qy 361 GGCAGTTTTGGAAAGGTTCTTCTAGCAAGACACAAGGCGAGAAAGTGTTCATGCAATC 420
Db 420 GGCAGTTTTGGAAAGGTTCTTCTAGCAAGACACAAGGCGAGAAAGTGTTCATGCAATC 479
Qy 421 AAAGTTTTCAGAGAAAGCAATCTCTGAAAAAGAAAGAGAGAGAGCAATATATGTCGGAG 480
Db 480 AAAGTTTTCAGAGAAAGCAATCTCTGAAAAAGAAAGAGAGAGCAATATATGTCGGAG 539
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481 CGGAATGTTCTGTTGAGAAATGTGAAGCACCCTTCTCTGTTGGGCTTCACTTCTCTTTC 540
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540 CGGAATGTTCTGTTGAGAAATGTGAAGCACCCTTCTCTGTTGGGCTTCACTTCTCTTTC 599
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541 CAGACTGCTGACAAATGTACTTGTCTCTAGACTACATTAATGTTGAGAGTTGTTCTAC 600
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600 CAGACTGCTGACAAATGTACTTGTCTCTAGACTACATTAATGTTGAGAGTTGTTCTAC 659
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601 CATCTCCAGAGGAAACGCTCTCTCTGGAACCAAGGCTCGTTTCTATGCTGTGAAATA 660
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660 CATCTCCAGAGGAAACGCTCTCTCTGGAACCAAGGCTCGTTTCTATGCTGTGAAATA 719
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661 GCAGTGCCTTGGCTACCTGATCTCACTGAAATCGTTTATAGAGACTTAAACCA-GA 719
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720 GCCAGTGCCTTGGCTACCTGATCTCACTGAAATCGTTTATAGAGACTTAAACCAAGGA 779
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720 GAATATTTTGTCTAGATTACACAGG--ACACATTTGCTCTTACTGACTTC-GGACTCTGCAA 776
|||||
780 GAATATTTTGTCTAGATTACACAGG--ACACATTTGCTCTTACTGACTTCGACTCTGCAA 839
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777 GGAGAA--CATTTGAACCAACAGCAGCAACATCCACTT 812
840 GGAGAAACCATTTGAACCAACAGCCCAACATCCCTT 877
|||||

RESULT 7
BQ934765 982 bp mRNA linear EST 21-AUG-2002
LOCUS AGENCOURT 8837001 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6429403
5', mRNA sequence.
ACCESSION BQ934765
VERSION BQ934765.1 GI:22350148
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 982)
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2617 row: i column: 20
High quality sequence stop: 683.
Location/Qualifiers
1..982
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6429403"
/clone_lib="NIH_MGC_101"
/tissue_types="epidermoid carcinoma, cell line"
/lab_hosts="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
XhoI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
254 a 251 c 240 g 236 t 1 others
BASE COUNT
ORIGIN
Query Match 55.8%; Score 746.4; DB 14; Length 982;

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Best Local Similarity 98.5%; Pred. No. 1.4e-200;
Matches 806; Conservative 0; Mismatches 6; Indels 6; Gaps 5;

QY 1 ATGGGGGAGATGAGAGGCGGCTGGCCAGAGCCGGCTCGAGTCCCTGCTGCGGCGCCCGC 60
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Db 14 ATGGGGGAGATGAGAGGCGGCTGGCCAGAGCCGGCTCGAGTCCCTGCTGCGGCGCCCGC 73
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QY 61 CACAAAAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
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Db 74 CACAAAAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 133
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QY 121 TTTCATGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
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Db 134 TTTCATGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 193
|||||
QY 181 TATGATGCAACACACCCCTGAAAGTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 240
|||||
Db 194 TATGATGCAACACACCCCTGAAAGTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 253
|||||
QY 241 GAGCTTATGATGCAACACCCCTTCTCTCCACCAAGTCTTCTCAGCAAAATCAACCTTGGC 300
|||||
Db 254 GAGCTTATGATGCAACACCCCTTCTCTCCACCAAGTCTTCTCAGCAAAATCAACCTTGGC 313
|||||
QY 301 CCGTCTGCAATCTCATGCTAAACCATCTGACTTTCACCTTCTTGAAGTGAATCGGAAAG 360
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Db 314 CCGTCTGCAATCTCATGCTAAACCATCTGACTTTCACCTTCTTGAAGTGAATCGGAAAG 373
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QY 361 GGAGTGTGGAAGGTTCTTAGCAAGACACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
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Db 374 GGAGTGTGGAAGGTTCTTAGCAAGACACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 433
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QY 421 AAGTGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
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Db 434 AAGTGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 493
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QY 481 CGGAATGTTCTGTTGAGAAATGTGAAGCACCCTTCTCTGTTGGGCTTCACTTCTCTTTC 540
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Db 494 CGGAATGTTCTGTTGAGAAATGTGAAGCACCCTTCTCTGTTGGGCTTCACTTCTCTTTC 553
|||||
QY 541 CAGACTGCTGACAAATGTACTTGTCTTAGACTACATTAATGTTGAGAGTTGTTCTAC 600
|||||
Db 554 CAGACTGCTGACAAATGTACTTGTCTTAGACTACATTAATGTTGAGAGTTGTTCTAC 613
|||||
QY 601 CATCTCCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
|||||
Db 614 CATCTCCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 673
|||||
QY 661 GCAGTGCCTTGGGCTACCTGCACTTCACTGAAACATCGTTTATAGAGACTTAAACCAAG 720
|||||
Db 674 GCAGTGCCTTGGGCTACCTGCACTTCACTGAAACATCGTTTATAGAGACTTAAACCAAG 733
|||||
QY 721 AATATTTGCTAGATTACAGAGG-ACACATTTG-CTTACTGAC-TTCGAGTCT-GCAA 776
|||||
Db 734 AATATTTGCTAGATTACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 793
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QY 777 GGAGACATTTGAACAA--CAGCACAACATCCACTT 812
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Db 794 GGAGACATTTGAACAA--CAGCACAACATCCACTT 831
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RESULT 8
LOCUS BQ934765
DEFINITION 603051130F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5191422 5',
mRNA sequence.
ACCESSION BQ934765
VERSION BQ934765.1 GI:15756574
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 851)
REFERENCE

```

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-x@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM1478 row: k column: 07
 High quality sequence start: 3
 High quality sequence stop: 756.

FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5191422"
 /clone_lib="NIH_MGC_116"
 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library."

BASE COUNT 215 a 225 c 199 g 212 t

ORIGIN

Query Match 54.6%; Score 730.2; DB 13; Length 851;
 Best Local Similarity 99.5%; Pred. No. 5.2e-196;
 Matches 743; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 592 TTGTTCTACCATCTCCAGAGGGAACGCTCTTCTCGAAGCACGCGGCTCGTTCTATGCT 651
 Db 1 TTGTTCTACCATCTCCAGAGGGAACGCTCTTCTCGAAGCACGCGGCTCGTTCTATGCG 60

QY 652 GCTGAATAGCAGTGCTCTGGGCTACCTGCATTCACCTGAACATCGCTTTATAGACTTA 711
 Db 61 GCTGAATAGCAGTGCTCTGGGCTACCTGCATTCACCTGAACATCGCTTTATAGACTTA 120

QY 712 AAACGAGAGATATTTTGTAGATTACAGGACACATTTGCTTACTGACTTCGGACTC 771
 Db 121 AAACGAGAGATATTTAGTAGATTACAGGACACATTTGCTTACTGACTTCGGACTC 180

QY 772 TGCAGGAGACATTGGAACACACAGACACATCCACCTCTGTGCGACGCGGAGTAT 831
 Db 181 TGCAGGAGACATTGGAACACACAGACACATCCACCTCTGTGCGACGCGGAGTAT 240

QY 832 CTGCACTCAGGTGCTTCTAAGCAGCTTTATGACAGGACTGTGGACTGGTGTGCTG 891
 Db 241 CTGCACTCAGGTGCTTCTAAGCAGCTTTATGACAGGACTGTGGACTGGTGTGCTG 300

QY 892 GGAGCTCTTGTATGAGATGCTGTATGGCTGCGGCTTTTATAGCCGAAACACAGCT 951
 Db 301 GGAGCTCTTGTATGAGATGCTGTATGGCTGCGGCTTTTATAGCCGAAACACAGCT 360

QY 952 GAAATGTACACACATCTTGACACAGCCTCTCCAGCTGAACCAATATACAAATTC 1011
 Db 361 GAAATGTACACACATCTTGAAACAGCCTCTCCAGCTGAACCAATATACAAATTC 420

QY 1012 GCAAGACACCTCTCGGAGGCTCTCTGCAGAGGACAGGACAAAGCGGCTCGGGCCAA 1071
 Db 421 GCAAGACACCTCTCGGAGGCTCTCTGCAGAGGACAGGACAAAGCGGCTCGGGCCAA 480

QY 1072 GATGACTTCATGGAGATTAAGAGTCATGTCTTCTTCTTAATTAACCTGGGATGATCTC 1131

Db 481 GATGACTTCATGGAGATTAAGAGTCATGTCTTCTTCTTAATTAACCTGGGATGATCTC 540
 QY 1132 ATTAATAAGAAGATTACTCCCTTTTAAACCCAAATGTAGTGGGCGCAACGACCTACGG 1191
 Db 541 ATTAATAAGAAGATTACTCCCTTTTAAACCCAAATGTAGTGGGCGCAACGACCTACGG 600
 QY 1192 CACTTTGACCCGAGTTTACCGAAGAGCCTGTGCCCAACTCCATTGGCAAGTCCCTGAC 1351
 Db 601 CACTTTGACCCGAGTTTACCGAAGAGCCTGTGCCCAACTCCATTGGCAAGTCCCTGAC 660
 QY 1252 AGCGTCTCGTCACAGCCGAGCTCAAGGAGCTCGGAGGCTTCTAGGCTTTCTCTAT 1311
 Db 661 AGCGTCTCGTCACAG-CAGCGTCAAGGAGCTCGGAGGCTTCTTAGGCTTTCTCTAT 719
 QY 1312 GCGCCTCCCAAGGACTCTTTCTCTCGA 1338
 Db 720 GCGCCTCCCAAGGACTCTTTCTCTCGA 746

RESULT 9
 AUI134278

LOCUS AUI134278 741 bp mRNA linear EST 01-AUG-2002
 DEFINITION AUI134278 OVARC1 Homo sapiens cDNA clone OVARC1001642 5', mRNA sequence.

ACCESSION AUI134278
 VERSION AUI134278.1 GI:10994817
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 741)
 AUTHORS Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
 TITLE HRI human cDNA project
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
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 /db_xref="taxon:9606"
 /clone="OVARC1001642"
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 /tissue_type="ovary, tumor tissue"
 /note="Vector: pME18SFL3"

BASE COUNT 209 a 168 c 179 g 182 t 3 others

ORIGIN

Query Match 53.3%; Score 712.8; DB 9; Length 741;
 Best Local Similarity 99.1%; Pred. No. 4.2e-191;
 Matches 736; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 343 TTCAAGTATCGGAAGGCGAGTTTGGAAAGGTTCTTCTAGCAGACACAGGCGAA 402
 Db 1 TTCAAGTATCGGAAGGCGAGTTTGGAAAGGTTCTTCTAGCAGACACAGGCGAA 60

QY 403 GAAGTCTTCTATGCACTCAAAAGTTTTCAGAGAAAGCAATCTGAAAAAGAGGAG 462
 Db 61 GAAGTCTTCTATGCACTCAAAAGTTTTCAGAGAAAGCAATCTGAAAAAGAGGAG 120

QY 463 AAGCATATTATGTCGGGCGGAATGTCTGTGGAAGATGTGAAGCACCCCTTTCTCTGGTG 522

121 AAGCATATATGTCGGAGCGGAATGTTCTGTTGAAGAATGTGAAGCACCTTCTTCGTG 180
122 AAGCATATATGTCGGAGCGGAATGTTCTGTTGAAGAATGTGAAGCACCTTCTTCGTG 180
523 GGCCTTCACTCTCTTTCCAGAGCTGTCGACAAATGTACTTGTCTCTAGACTACATTAAT 582
524 GGCCTTCACTCTCTTTCCAGAGCTGTCGACAAATGTACTTGTCTCTAGACTACATTAAT 582
181 GGCCTTCACTCTCTTTCCAGAGCTGTCGACAAATGTACTTGTCTCTAGACTACATTAAT 240
182 GGCCTTCACTCTCTTTCCAGAGCTGTCGACAAATGTACTTGTCTCTAGACTACATTAAT 240
583 GGTGGAGAGTTGTTCTACCATCTCCAGAGGAGCGCTGCTTCTCTGGAACACACGGGCTCGT 642
584 GGTGGAGAGTTGTTCTACCATCTCCAGAGGAGCGCTGCTTCTCTGGAACACACGGGCTCGT 642
241 GGTGGAGAGTTGTTCTACCATCTCCAGAGGAGCGCTGCTTCTCTGGAACACACGGGCTCGT 300
242 GGTGGAGAGTTGTTCTACCATCTCCAGAGGAGCGCTGCTTCTCTGGAACACACGGGCTCGT 300
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301 TTCTATGCTGCTGAAATAGCCAGTGCCTTGGGCTACCTGCAATTCACATGAAACATCGTTTAT 360
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703 AGAGACTTAAACACAGAGAAATATTTGCTAGATTCACAGGAGACATGTCCTTACTGAC 762
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361 AGAGACTTAAACACAGAGAAATATTTGCTAGATTCACAGGAGACATGTCCTTACTGAC 420
362 AGAGACTTAAACACAGAGAAATATTTGCTAGATTCACAGGAGACATGTCCTTACTGAC 420
763 TTGGGACTCTGCAAGGAGAAATGAAACACAGAGCAACATCCACCTTCTGTGGCAGC 822
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421 TTGGGACTCTGCAAGGAGAAATGAAACACAGAGCAACATCCACCTTCTGTGGCAGC 480
422 TTGGGACTCTGCAAGGAGAAATGAAACACAGAGCAACATCCACCTTCTGTGGCAGC 480
823 CCGGAGTATCTCGACCTGAGGCTTCTATAAGCAGCCTTATGACAGGACTGTGGACTGG 882
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481 CCGGAGTATCTCGACCTGAGGCTTCTATAAGCAGCCTTATGACAGGACTGTGGACTGG 540
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883 TGTGCTCTGGAGCTGCTTGTATGAGATGCTGTATGAGCTGCGGCTTTTATAGCCGA 942
884 TGTGCTCTGGAGCTGCTTGTATGAGATGCTGTATGAGCTGCGGCTTTTATAGCCGA 942
541 TGTGCTCTGGAGCTGCTTGTATGAGATGCTGTATGAGCTGCGGCTTTTATAGCCGA 600
542 TGTGCTCTGGAGCTGCTTGTATGAGATGCTGTATGAGCTGCGGCTTTTATAGCCGA 600
943 AACACAGCTGAAATGTAGCAACATTTCTGAACAGCCTTCCAGCTGGAACCAATATT 1002
944 AACACAGCTGAAATGTAGCAACATTTCTGAACAGCCTTCCAGCTGGAACCAATATT 1002
601 AACACAGCTGAAATGTAGCAACATTTCTGAACAGCCTTCCAGCTGGAACCAATATT 660
602 AACACAGCTGAAATGTAGCAACATTTCTGAACAGCCTTCCAGCTGGAACCAATATT 660
1003 ACAAATCCGACAGACCTCTCTGGAGGCGCTCTCGAGAGGACAGGACAAAGCGGCTC 1062
1004 ACAAATCCGACAGACCTCTCTGGAGGCGCTCTCGAGAGGACAGGACAAAGCGGCTC 1062
661 ACAAATCCGACAGACCTCTCTGGAGGCGCTCTCGAGAGGACAGGACAAAGCGGCTC 718
662 ACAAATCCGACAGACCTCTCTGGAGGCGCTCTCGAGAGGACAGGACAAAGCGGCTC 718
1063 GGGGCCAAGATGATCTCATGGA 1085
1064 GGGGCCAAGATGATCTCATGGA 1085
719 GGGGCCAAGATGATCTCATGGA 741

RESULT 10
BG575325
LOCUS 602597986F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4706829 5',
DEFINITION mRNA sequence.
ACCESSION BG575325
VERSION BG575325.1 GI:13582978
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 736)
NIH-MGC <http://mhc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL0575 row: k column: 22
High quality sequence stop: 732.
Location/Qualifiers
1. 736

FEATURES
Source

/organism="Homo sapiens"
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/issue_type="mammary adenocarcinoma, cell line"
/lab_host="PH10B (phage-resistant)"
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Site 2: SalI; Cloned unidirectionally; oligo-dT-primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: This is a NIH MGC Library."
BASE COUNT 186 a 205 c 168 g 177 t
ORIGIN
Query Match 53.0%; Score 709.8; DB 12; Length 736;
Best Local Similarity 98.8%; Pred. No. 3e-190;
Matches 726; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
QY 604 CTCAGAGGGAACGCTGCTTCTCTGGAACCAACGCGGCTCGTTTCTATGCTGCTGAAATAGCC 663
DB 1 CTCAGAGGGAACGCTGCTTCTCTGGAACCAACGCGGCTCGTTTCTATGCTGCTGAAATAGCC 60
QY 664 AGTGCCTTGGGCTACCTGCAATTCACATGAAATCGTTTATAGAGACTTAAACACAGAGAAT 723
DB 61 AGTGCCTTGGGCTACCTGCAATTCACATGAAATCGTTTATAGAGACTTAAACACAGAGAAT 120
QY 724 ATTTGCTAGATTCACAGGAGACATTTGCTTCTTCTGACTTCTGCAAGGAGAAC 783
DB 121 ATTTGCTAGATTCACAGGAGACATTTGCTTCTTCTGACTTCTGCAAGGAGAAC 180
QY 784 ATTGAACACAAACAGCAACATCCACCTTCTGTGGCAACCGCGAGTATCTCGACCTGAG 843
DB 181 ATTGAACACAAACAGCAACATCCACCTTCTGTGGCAACCGCGAGTATCTCGACCTGAG 240
QY 844 GTGCTTTCATAAGCAGCCTTATGACAGGACTGTGGAGCTGTGGTGTGCTGGAGCTGTCTTG 903
DB 241 GTGCTTTCATAAGCAGCCTTATGACAGGACTGTGGAGCTGTGGTGTGCTGGAGCTGTCTTG 300
QY 904 TATGAGATGCTGTATGGCTGCGGCTTTTATAGCGGAACACAGCTGAAATGTAGGAC 963
DB 301 TATGAGATGCTGTATGGCTGCGGCTTTTATAGCGGAACACAGCTGAAATGTAGGAC 360
QY 964 AACATTCTGAACAAAGCTCTCCAGCTGAAACCAATATTACAAATTCGCAAGACACCTC 1023
DB 361 AACATTCTGAACAAAGCTCTCCAGCTGAAACCAATATTACAAATTCGCAAGACACCTC 420
QY 1024 CTGAGGCGCTCTGAGAGGACAGGACAAAGCGCTCGGGCCCAAGGATGACTTCATG 1083
DB 421 CTGAGGCGCTCTGAGAGGACAGGACAAAGCGCTCGGGCCCAAGGATGACTTCATG 480
QY 1084 GAGATTAAAGATCATGCTTCTTCTCTTAATTAACCTGGGATGATCTCATTAATAGAAG 1143
DB 481 GAGATTAAAGATCATGCTTCTTCTCTTAATTAACCTGGGATGATCTCATTAATAGAAG 540
QY 1144 ATTACTCCCCCTTTTAAACCAATATGTAGTGGGCCCAACAGCTAGGGACTTTGACCCC 1203
DB 541 ATTACTCCCCCTTTTAAACCAATATGTAGTGGGCCCAACAGCTAGGGACTTTGACCCC 600
QY 1204 GAGTTTACGGAAGAGCTGTCCCAACTCAATTTGGCAAGTCCCTGACAGCGCTCGTGC 1263
DB 601 GAGTTTACGGAAGAGCTGTCCCAACTCAATTTGGCAAGTCCCTGACAGCGCTCGTGC 660
QY 1264 ACAGCAGGCTCAAGAGCTGCGGAGCTTCTTAGGCTTTTCTTATGCGCTCCACG 1323
DB 661 ACAGC--AGCGTCAGGAAGCTGCCGAGGCTTTCTTAGGCTTTTCTTATGCGCTCCACG 718
QY 1324 GACTCTTCTCTGTA 1338
DB 719 GACTCTTCTCTGTA 733
RESULT 11
ALS30006

LOCUS AL530006 811 bp mRNA linear EST 13-FEB-2001
 DEFINITION AL530006 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD009YH16 5
 prime, mRNA sequence.
 ACCESSION AL530006
 VERSION AL530006.1 GI:12793499
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 811)
 AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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 /lab_host="DH10B"
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 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed
 by Life Technologies. Contact : Feng Liang Life
 Technologies, a division of Invitrogen 9800 Medical Center
 Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
 8371 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 221 a 200 c 180 g 210 t
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 Best Local Similarity 99.9%; Pred. No. 1.5e-189;
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 969)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
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 http://image.llnl.gov
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 Average insert size 1.4 kb. Library prepared by Life
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Db      TCTGTGACGCGGAGATCTCGACCTGAGGTGCTTCAAGAGCCCTTATGACAGGA 240
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VERSION     BM460788.1
KEYWORDS    GI:18509828
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1070)
AUTHORS     NIH-MGC http://mgi.nci.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
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Best Local Similarity 91.7%; Pred. No. 4.2e-188;
Matches 856; Conservative 0; Mismatches 59; Indels 18; Gaps 10;
QY      116 TGCTTTTCATGAAGCAGAGGAGGATGGGTCTGAACACATTTTATTCAGAGATTGCCAATA 175
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 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library." |

BASE COUNT 221 a 210 c 196 g 217 t 1 others
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Query Match 52.2%; Score 698.4; DB 12; Length 845;

Best Local Similarity 97.4%; Pred. No. 5.7e-187;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	527.2	39.4	1456	9	US-10-119-926-20
7	527.2	39.4	1812	10	US-09-971-118-1
8	520.4	38.9	2512	10	US-09-784-249-1
9	517.2	38.7	2760	9	US-10-098-841-195
10	410.4	30.7	423	10	US-09-925-300-860
11	383.4	28.7	447	9	US-09-918-995-15481
12	351.6	26.3	851	9	US-09-764-868-56
13	322.8	24.1	476	9	US-09-918-995-13695
14	263.4	19.7	404	10	US-09-960-352-7426
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ALIGNMENTS

RESULT 1

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; Sequence 6, Application US/09810808
; Patent No. US20020042114A1
; GENERAL INFORMANT:
; APPLICANT: Au-Young, Janice
; Guegler, Karl J.
; Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/810,808
; FILING DATE: 15-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/541,228
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

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; IMMEDIATE SOURCE:
; LIBRARY: <Unknown>
; CLONE: Consensus
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-810-808-6

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 416 CAGTCAAAAGTTTACAGAAAGAGCAATCTGAAAGAAAGAGAGGAGCAATATATGT 475
DB 383 CAGTCAAAAGTTTACAGAAAGAGCAATCTGAAAGAAAGAGAGGAGCAATATATGT 442
QY 476 CGGAGCGGAATGTCTGTTGAAGAAATGTGAAGACACCTTTCTGGTGGGCTTCACTTCT 535
DB 443 CGGAGCGGAATGTCTGTTGAAGAAATGTGAAGACACCTTTCTGGTGGGCTTCACTTCT 502
QY 536 CTTTCCAGACTGCTGACAAATGTACTTTGTCTAGACTACATTAATGTTGGAGAGTGT 595
DB 503 CTTTCCAGACTGCTGACAAATGTACTTTGTCTAGACTACATTAATGTTGGAGAGTGT 562
QY 596 TCTACCACTCTCCAGAGGGAAGCGTCTCTCTGGAACCAACCGGCTCGTTTCTATGCTGCTG 655
DB 563 TCTACCACTCTCCAGAGGGAAGCGTCTCTCTGGAACCAACCGGCTCGTTTCTATGCTGCTG 622
QY 656 AATATAGCCAGTGTCTGGGTACTCTGATTCATCTGAACATCGTTTATATAGAGACTTAAAC 715
DB 623 AATATAGCCAGTGTCTGGGTACTCTGATTCATCTGAACATCGTTTATATAGAGACTTAAAC 682
QY 716 CAGAGAAATATTTGCTAGATTTCAGGGGACACATTTGCTTACTGACTTCGGACTCTGCA 775
DB 683 CAGAGAAATATTTGCTAGATTTCAGGGGACACATTTGCTTACTGACTTCGGACTCTGCA 742
QY 776 AGAGAAACATTTGAACACAAACAGCACATCCACCTTCTGTGGCACCCCGGAGTATCTCG 835
DB 743 AGAGAAACATTTGAACACAAACAGCACATCCACCTTCTGTGGCACCCCGGAGTATCTCG 802
QY 836 CACTGAGGTGCTTTCATAGCAGCGCTTATGACAGGACTGTGGACTGTGTGCTGGGAG 895
DB 803 CACTGAGGTGCTTTCATAGCAGCGCTTATGACAGGACTGTGGACTGTGTGCTGGGAG 862
QY 896 CTGTCTTGTATGAGATGCTGTATGGCTGCGGCTTTTATAGCCGAAACACAGCTGAAA 955
DB 863 CTGTCTTGTATGAGATGCTGTATGGCTGCGGCTTTTATAGCCGAAACACAGCTGAAA 922
QY 956 TGTACGACAAATTTGAAACAAAGCTCTCCAGCTGAAACCAAAATATTTACAAATTCGCA 1015
DB 923 TGTACGACAAATTTGAAACAAAGCTCTCCAGCTGAAACCAAAATATTTACAAATTCGCA 982
QY 1016 GACACTCTCGAGGGCTCTCTGCAAGAGGACAGGACAAAGCGGCTCGGGGCCAAGATG 1075
DB 983 GACACTCTCGAGGGCTCTCTGCAAGAGGACAGGACAAAGCGGCTCGGGGCCAAGATG 1042

RESULT 2
US-09-981-353-6
; Sequence 6, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Laeek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 2365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 3819039CBI
US-09-981-353-6

Query Match          91.2%; Score 1219.8; DB 9; Length 2365;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 116 TGGCTTTCATGAAGCAGAGAGAGATGGTCTGAACGACTTTATTCAGAGAGATTGCCAATA 175
DB 134 TGGCTTTCATGAAGCAGAGAGAGATGGTCTGAACGACTTTATTCAGAGAGATTGCCAATA 193
QY 176 ACTCCATATGATCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235
DB 194 ACTCCATATGATCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 253
QY 236 AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTCTTCAGCAAAATCAACC 295
DB 254 AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTCTTCAGCAAAATCAACC 313
QY 296 TTGGCCCGTCTGCTCAATCTCATGCTAAACCATCTGACTTTTCACTTTTGAAGTGTATG 355
DB 314 TTGGCCCGTCTGCTCAATCTCATGCTAAACCATCTGACTTTTCACTTTTGAAGTGTATG 373
QY 356 GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAGACACAAGGCGAGAGAGTGTCTATG 415
DB 374 GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAGACACAAGGCGAGAGAGTGTCTATG 433
QY 416 CAGTCAAAAGTTTACAGAAAGAGCAATCTGAAAGAAAGAGAGGAGCAATATATGT 475
DB 434 CAGTCAAAAGTTTACAGAAAGAGCAATCTGAAAGAAAGAGAGGAGCAATATATGT 493
QY 476 CGGAGCGGAATGTCTGTTGAAGAAATGTGAAGACACCCCTTTCTCTGGTGGGCTTCTACTTCT 535
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Db 494 CGGAGCGGATGTTCTTTGAAGATGTGAAGCACCCCTTTCTGGTGGGCTTCACTTCT 553
Qy 536 CTTTCCAGACTGCTGACAAATTTGACTTTGCTCTAGACTACATTAATGTTGGAGATTGT 595
Db 554 CTTTCCAGACTGCTGACAAATTTGACTTTGCTCTAGACTACATTAATGTTGGAGATTGT 613
Qy 596 TCTACCAATCTCAGAGGAAACGCTGCTTCTGGAACACCGGGCTGTTTCTATGCTGCTG 655
Db 614 TCTACCAATCTCAGAGGAAACGCTGCTTCTGGAACACCGGGCTGTTTCTATGCTGCTG 673
Qy 656 AATAGCAGCTGCTGGGCTACTGCTGATTCATTCAGTCAATCGTTTATAGAGACTTAAAC 715
Db 674 AATAGCAGCTGCTGGGCTACTGCTGATTCATTCAGTCAATCGTTTATAGAGACTTAAAC 733
Qy 716 CAGAGAATATTTGCTAGATTTCAGGGACACATTTGCTTACTGACTTCGGACTCTGCA 775
Db 734 CAGAGAATATTTGCTAGATTTCAGGGACACATTTGCTTACTGACTTCGGACTCTGCA 793
Qy 776 AGGAGAACATTGAACACAAAGCAGACATTCACCTTTCTGTGGACGCGGAGTATCTCG 835
Db 794 AGGAGAACATTGAACACAAAGCAGACATTCACCTTTCTGTGGACGCGGAGTATCTCG 853
Qy 836 CACTGAGTGCTTCATAAGCAGCTTATGACAGGACTGTGGACTGGTGGCTCTGGGAG 895
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Db 1034 GACACTCTCGAGGGCTCTCGAAGACAGGACAAAGCGCTCGGGGCCAAGGATG 1093
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Db 1214 TTGACCCGAGTTTACCGAAGAGCTGTCCCAACTCCATTTGGCAAGTCCCTTGACAGCG 1273
Qy 1256 TCCTCGTCACAGCAGGCTCAAGAGCTGCCGAGGCTTTCTAGGCTTTTCTATGCGC 1315
Db 1274 TCCTCGTCACAGCAGGCTCAAGAGCTGCCGAGGCTTTCTAGGCTTTTCTATGCGC 1333
Qy 1316 CTCCACGAGCTCTTCTCTCTGA 1338
Db 1334 CTCCACGAGCTCTTCTCTCTGA 1356
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RESULT 3

US-10-000-039-1

; Sequence 1, Application US/10000039

; Publication No. US20030003559A1

; GENERAL INFORMATION:

; APPLICANT: LANG, Florian

; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY & LARDNER

; STREET: 3000 K Street, N.W.

; CITY: Washington

```
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/000,039
; FILING DATE: 04-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,295
; FILING DATE: 26-FEB-1998
; APPLICATION NUMBER: DE 197-08-173.8
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanderscock, Collin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 058315/0123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2370 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1335
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-10-000-039-1
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Query Match 91.0%; Score 1218.2; DB 9; Length 2370;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 116 TGGCTTTTATGAAGCAGAGGAGGATGGGTCTGAACACTTTTATTCAGAGATTGCCAATA 175
Db 116 TGGCTTTTATGAAGCAGAGGAGGATGGGTCTGAACACTTTTATTCAGAGATTGCCAATA 175
Qy 176 ACTCCTATCATGACCAACACCTGAGTTTCAGTCCATCTTGAGATCTCCCACTCAGG 235
Db 176 ACTCCTATCATGACCAACACCTGAGTTTCAGTCCATCTTGAGATCTCCCACTCAGG 235
Qy 236 AGCCTGAGCTTATGAATGCCAACCTTCTCTCCCAAGTCTCTTCAGCAATCAACC 295
Db 236 AGCCTGAGCTTATGAATGCCAACCTTCTCTCCCAAGTCTCTTCAGCAATCAACC 295
Qy 296 TTGGCCCGTCGTCCTAATCTCATGTAAACCATCTGACTTTTCACTTTTGAAGTATCG 355
Db 296 TTGGCCCGTCGTCCTAATCTCATGTAAACCATCTGACTTTTCACTTTTGAAGTATCG 355
Qy 356 GAAAGGCGAGTTTGGAGAGGTTCTTCTAGCAGACACAAAGCAGAGAGTGTCTCTATG 415
Db 356 GAAAGGCGAGTTTGGAGAGGTTCTTCTAGCAGACACAAAGCAGAGAGTGTCTCTATG 415
Qy 416 CAGTCAAAAGTTTTACAGAAAGCAATCTCGAAAGAAAGAGAGAGCATATTATGT 475
Db 416 CAGTCAAAAGTTTTACAGAAAGCAATCTCGAAAGAAAGAGAGAGCATATTATGT 475
Qy 476 CGGAGCGGAATGTTCTGTTGAAAGATGTGAAGCACCCCTTCTGTTGGGCTTCACTTCT 535
Db 476 CGGAGCGGAATGTTCTGTTGAAAGATGTGAAGCACCCCTTCTGTTGGGCTTCACTTCT 535
Qy 536 CTTTCCAGACTGCTGACAAATTTGTACTTTTGTCTAGACTACATTATATGTTGGAGATTGT 595
Db 536 CTTTCCAGACTGCTGACAAATTTGTACTTTTGTCTAGACTACATTATATGTTGGAGATTGT 595
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956 TGTACGACAACTTCTGAAACAGCCTCTCCAGCTGAAACCAAAATATTACAAATTTCCGCAA 1015
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1076 ACTTCATGAGATTAAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1135
1076 ACTTCATGAGATTAAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1135
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1196 TTAGCCCGAGTTTACGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1255
1256 TCCTGTCAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1315
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1316 CTCCACGAGCTCTTCTCTCTGA 1338
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RESULT 4
US-09-969-347-214
; Sequence 214, Application US/09969347
; Patent No. US20020115085A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-69
; CURRENT APPLICATION NUMBER: US/09/969,347
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,598
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,604
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 318
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 214
; LENGTH: 2370
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-09-969-347-214
Query Match 91.0%; Score 1218.2; DB 10; Length 2370;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 116 TGGCTTTTCATGAAGCAGAGGAGGATGGGCTCAGACGACTTTATTCAGAGAGATTGCCAATA 175
DB 116 TGGCTTTTCATGAAGCAGAGGAGGATGGGCTCAGACGACTTTATTCAGAGAGATTGCCAATA 175
QY 176 ACTCTCTATGATCATGCAACACACCTCTGAAAGTTTCACTGTCATCTTGAAGATCTCCCAACCTCAGG 235
DB 176 ACTCTCTATGATCATGCAACACACCTCTGAAAGTTTCACTGTCATCTTGAAGATCTCCCAACCTCAGG 235
QY 236 AGCTGAGCTTATGAATGCAACACCTCTCTCTCCACCAAGTCTCTCTCAGCAAAATCAACC 295
DB 236 AGCTGAGCTTATGAATGCAACACCTCTCTCTCCACCAAGTCTCTCTCAGCAAAATCAACC 295
QY 296 TTGGCCCGCTGCTCCCAATCTCATGCTAAACCATCTGACTTTTCACTTTCTTTGAAAGTGTATCG 355
DB 296 TTGGCCCGCTGCTCCCAATCTCATGCTAAACCATCTGACTTTTCACTTTCTTTGAAAGTGTATCG 355
QY 356 GAAAGGCGAGTTTGGAAAGGTTTCTTCTAGCAAGACACAAGGCGAGAGAGTGTCTTCTATG 415
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DB 476 CGGAGCGGAGTGTCTGTTGAAAGATGTGAAGCAGCCTTTCTCTGGTGGGCTTCACTTCT 535
QY 536 CTTTCCAGAGCTGCTGCAAAATTTGACTTTTCTCTAGACTACATTAATGTTGGAGAGTGT 595
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DB 716 CAGAGAAATATTTGCTAGATTTTCAAGGAGACATTTGCTTACTGACTTCGGACTCTGCA 775
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DB 776 AGGAGAAATATTTGCTAGATTTTCAAGGAGACATTTGCTTACTGACTTCGGACTCTGCA 835
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DB 956 TGTACGACAACTTCTGAAACAGCCTCTCCAGCTGAAACCAAAATATTACAAATTTCCGCAA 1015
QY 1016 GACACTCTCTGGAGGCTCTCTGAGAGGACGACGACGACGACGACGACGACGACGACGAC 1075
DB 1016 GACACTCTCTGGAGGCTCTCTGAGAGGACGACGACGACGACGACGACGACGACGACGAC 1075
QY 1076 ACTTCATGAGATTAAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1135
DB 1076 ACTTCATGAGATTAAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1135

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Db 1076 ACTTCATGGAGATTAAGAGTCATGCTCTTCTCTCTTAATTAACCTGGAGTATCTCATTA 1135
Qy 1136 ATAAGAGATTAATCTCCCTTTTAAACCAATGTGAGTGGGCCCAACGACCTACGGCACT 1195
Db 1136 ATAAGAGATTAATCTCCCTTTTAAACCAATGTGAGTGGGCCCAACGAGCTACGGCACT 1195
Qy 1196 TTGACCCGAGTTTACCGAAGAGCTGTCCCAACTCCATTGGCAAGTCCCTGACAGCG 1255
Db 1196 TTGACCCGAGTTTACCGAAGAGCTGTCCCAACTCCATTGGCAAGTCCCTGACAGCG 1255
Qy 1256 TCCTCGTCACAGCCAGGCTCAAGGAAGCTGCCGAGGCTTTCTAGGCTTTTCTATGGC 1315
Db 1256 TCCTCGTCACAGCCAGGCTCAAGGAAGCTGCCGAGGCTTTCTAGGCTTTTCTATGGC 1315
Qy 1316 CTCCACGGACTCTTTCTCTGA 1338
Db 1316 CTCCACGGACTCTTTCTCTGA 1338

RESULT 5

US-09-880-107-3855
; Sequence 3855, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3855
; LENGTH: 2370
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 Y10032
US-09-880-107-3855

Query Match 91.08; Score 1218.2; DB 10; Length 2370;
Best Local Similarity 99.88; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 116 TGGCTTTTCATGAAGCAGAGGAGGATGGTCTGAACGACTTTATTTCAGAAGATTGCCAATA 175
Db 116 TCGCTTTTCATGAAGCAGAGGAGGATGGTCTGAACGACTTTATTTCAGAAGATTGCCAATA 175
Qy 176 ACTCTATGATGCAACACCTGAAAGTTGAGTCCATCTTGAAGATCTGCCAACCTCAGG 235
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Qy 236 AGCTGAGCTTATGAATGCCAACCTCTCTCTCCACCAAGTCTTCTCAGCAATCAACC 295
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Db 416 CAGTCAAGTGTATACAGAAAGAGCATCTCTGAAAGAGAGGAGAGCATATTATGT 475

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Db 476 CGGAGCGGAATGTTCTGTTGAAGATGTGAAGCACCCCTTTCTGGTGGGCTTTCACCTCT 535
Qy 536 CTTTCCAGACTGCTGACAAATTTGTACTTTCTCTAGACTACATTAATGTTGGAGAGTGT 595
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Db 596 TCTACCATCTCCAGAGGAAACGCTGCTTCTGGAACCAACGCGCTCGTTTCTATGCTGCTG 655
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Db 656 AAATAGCCAGTGGCTTGGGCTACCTGCAATTCATCTGAACATCGTTTATAGAGACTTAAAC 715
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Db 1256 TCCTCGTCACAGCCAGGCTCAAGGAAGCTGCCGAGGCTTTCTAGGCTTTTCTATGCGC 1315
Qy 1316 CTCCACGGACTCTTTCTCTGA 1338
Db 1316 CTCCACGGACTCTTTCTCTGA 1338

RESULT 6

US-10-119-926-20
; Sequence 20, Application US/10119926
; Publication No. US20030104413A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhao, Qing A.

```
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Xu, Chongjun
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104413A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 789CIP2BCON
; CURRENT APPLICATION NUMBER: US/10/119,926
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 20
; LENGTH: 1456
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (217)..(1320)
US-10-119-926-20

Query Match 39.4%; Score 527.2; DB 9; Length 1456;
Best Local Similarity 69.5%; Pred. No. 1.7e-159;
Matches 734; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

Qy 261 TTCTCCTCCACCAAGTCTTCTCAGCAATCAACCTTGGCCGCTCGTCCCAATCCTCATGC 320
Db 246 TCCACAGCCCTCCAGGCCAATGGAACATCAACCTGGGCGCTTCAGCCAAACCAATGC 305
Qy 321 TAAACCATCTGACTTTCACCTTCTTGAAGTGATCGGAAGGGCAGTTTTCGAAAGGTCT 380
Db 306 CCAGCCACGGACTTTCACCTTCTTGAAGTGATCGGAAGGGCAGTTTTCGAAAGGTCT 365
Qy 381 TCTAGCAAGACACAAGCGAGAGAGTGTCTATGCAAGTCAAGTGTTCGAAAGTTCAGAAAGC 440
Db 366 ACTGGCCAAAGCGCAAGTCTGATGGGCGTCTATGCAAGTCAAGTGTTCGAAAGTTCAGAAAGC 425
Qy 441 AATCCTCAAAAGAAAGAGAGAGAGATATATGTCGAGCGGAAGTCTGTGTGAAGAA 500
Db 426 CATCTTAAAGAAAGAGAGAGAGAGATATATGTCGAGCGGAAGTCTGTGTGAAGAA 485
Qy 501 TGTGAAGCACCCCTTCTCTGTGGGCTTCACTTCTTCCAGACTGCTGACAAATGTGA 560
Db 486 CGTGCGGACCCCTTCTCTGTGGGCTTCACTTCTTCCAGACTGCTGACAAATGTGA 545
Qy 561 CTTTGTCTAGACTACATTAATGTGTGAGAGTGTCTTACATCTCCAGAGGGAACGCTG 620
Db 546 CTTGTGTCTGACTATGATCAACGGGGGAGAGCTTCTTCCACCTGAGCGGGAGCGCG 605
Qy 621 CTTTCTCGAACACCGGCTGTCTTCTATGCTGCTGAATAGCCAGTCCCTGGCTACCT 680
Db 606 GTTCTCTGGAGCCCGGGCCAGGTTCTACGCTGCTGAGGTGCGCCAGCGCCATTGGCTACCT 665
Qy 681 GCATTCTACTGAACATCGTTTATAGAGACTTAAACACAGAGAATATTTTGTAGATTACA 740
Db 666 GCATCTCTCAACATCATTTACAGGATCTGAACACAGAGACATTTCTTGTGAGTCCCA 725
Qy 741 GGGACACATGTGCTCTTACTGACTTTCGACTCTGCAAGAGAGAACATTTGAACACACAGCAC 800
Db 726 GGGACACGTGTGTGACGATTTTGGCTCTGCAAGAGAGAGGTGTAGAGCTCTGAAGACAC 785
Qy 801 AACATCCACCTTCTGCGACCGCGGAGTATCTGCACTCTGAGTGTCTTATAGAGACC 860
Db 786 CACATCCACATCTTGTGTGATCCCTGAGTACTTGGCACCTGAGTGTCTCGAAAGAGCC 845
Qy 861 TTATGACAGGACTGTGGAGCTGGTGGTGGTGGAGCTGTCTGTGTATGAGATGCTGTATGG 920
Db 841 TTATGATCGAGCAGTGGAGCTGGTGGTGGTGGGCGAGTCTCTTACGAGATGCTCCATGG 905
Qy 921 CCTGCCGCTTTTATAGCCGAAACACACAGCTGAATGTACGACCAATCTTGAACAGCC 980
Db 906 CCTGCCGCTTTTATAGCCGAAAGATGATCCAGATGTATGAGAACATTTCTGACCAGCC 965
Qy 981 TCTCCAGCTGAAACCAATATTACAAATTTCCGCAAGACACCTCTCTGGAGGCGCTCTCTGCA 1040
Db 966 GTTACAGATCCCGGAGCGGACAGTGGCGGCTGTGACCTCTCTCAAAAGCTTCTTCCA 1025
Qy 1041 GAAGGACAGACAAAGCGCTCGGGCCAAAGGATGCTTCTATGAGATTAAGAGTCAATGT 1100
Db 1026 CAAGGACAGACAGAGCGCTGGGCTCCAAAGCAGAGCTTCTTGTAGATTAAGAACATGT 1085
Qy 1101 CTTCTTCTCTTAATTAAGTGGATGATCTCATTATAGAGATTTACTCCCTCTTTTAA 1160
Db 1086 ATTCTTTCAGCCCAATTAAGTGGATGATCTTACCAAGAGAGGCTTAACCTCCACCTTCAA 1145
Qy 1161 CCCAAATGTAGTGGGCGCCAAAGCCTAGCGCACTTTGACCCCGAGTTTACCGAAGAGCC 1220
Db 1146 CCCAAATGTAGCAGGACCTGCTGACTTGAAGCATTTTGACCCAGAGTTTACCCAGGAGC 1205
Qy 1221 TGTCCCAACTCAATTTGGCAAGTCCCTGACAGCGTCTCTGTCACAGCGAGCTCAAGGA 1280
Db 1206 TGTGTCCAAAGTCCATTTGGCTGTACCCCTGACACTGT-----GCCCAGCAGCTCTGG 1256
Qy 1281 AGCTGCCGAGGCTTTCTTAGGCTTTTCTCTATGCGCC 1316
Db 1257 GGCCTCAAGTGCATTTCTGGGATTTTCTTATGCGCC 1292

RESULT 7
US-09-971-118-1
; Sequence 1, Application US/09971118
; Patent No. US20020123056A1
; GENERAL INFORMATION:
; APPLICANT: DELANEY, ALLEN
; APPLICANT: YOGANATHAN, THILLAINATHAN
; TITLE OF INVENTION: SGK2 AND ITS USES
; FILE REFERENCE: KINE025CIP
; CURRENT APPLICATION NUMBER: US/09/971,118
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/21479
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/237,419
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-971-118-1

Query Match 39.4%; Score 527.2; DB 10; Length 1812;
Best Local Similarity 69.5%; Pred. No. 2e-159;
Matches 734; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

Qy 261 TTCTCCTCCACCAAGTCTTCTCAGCAATCAACCTTGGCCGCTCGTCCCAATCCTCATGC 320
Db 117 TCCACAGCCCTCCAGGCCAATGGAACATCAACCTGGGCGCTTTCAGCCAAACCAATGC 176
Qy 321 TAAACCATCTGACTTTCACCTTCTTGAAGTGATCGGAAGGGCAGTTTTCGAAAGGTCT 380
Db 177 CCAGCCACGGACTTTCGACTTCTTCAAGTCTCGGCAAGGGAAGTCTACGGGAGGTCT 236
Qy 381 TCTAGCAAGACACAAGCGAGAGAGTGTCTTATGAGTCAAGTCAAGTCTTGAAGAGAAC 440
Db 237 ACTGGCCAGCGAGTCTGATGGGCGTCTATGAGTCAAGTCAAGTCTACAGAAAGATC 296
Qy 441 AATCCTCAAAAGAAAGAGAGAGAGATATTTATGTCGAGCGGGAATTTCTGTGTGAAGAA 500
Db 297 CATCTTAAAGAAAGAGAGAGAGAGATATTTATGTCGAGCGGAGTGTGTGTCTTGAAGAA 356
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Db 1454 ACCAGATGATACAGAACTTTGACACAGCAATTTACAGAGAAACAGTTCCATATCTGT 1513
 Qy 1236 TGGCAAGTCCCTGACAGCGTCTCTGTCACAGCCAGGTCAGAGAGCTCCGAGGCTTT 1295
 Db 1514 GTGTGTATCTTCTGACTATTTCTATAGTGAATGCCAGTGTATTGGAGCGCATGATGCATT 1573
 Qy 1296 CCTAGGCTTTTCTCTATCGCTCCACCGGA 1325
 Db 1574 CGTTGGTTTCTCTATGCACTCTCTTCAGA 1603

RESULT 9

US-10-098-841-195
 ; Sequence 195, Application US/10098841
 ; Publication No. US20020197679A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Xu, Chongjun
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Ma, Yunding
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Qian, Xiaohong B.
 ; APPLICANT: Drmanac, Radoje T.
 ; TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
 ; FILE OF INVENTION: Polypeptides
 ; FILE REFERENCE: 784CIP2
 ; CURRENT APPLICATION NUMBER: US/10/098,841
 ; CURRENT FILING DATE: 2002-03-13
 ; PRIOR APPLICATION NUMBER: 09/598,042
 ; PRIOR FILING DATE: 2000-06-20
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 331
 ; SOFTWARE: Pf_Fl_genes Version 1.0
 ; SEQ ID NO 195
 ; LENGTH: 2760
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (260)..(1750)
 ; US-10-098-841-195

Query Match 38.78; Score 517.2; DB 9; Length 2760;
 Best Local Similarity 88.38; Pred. No. 4.6e-156;
 Matches 71; Conservative 0; Mismatches 333; Indels 0; Gaps 0;
 Qy 276 TCCTTCTCAGCAATCAACCTTGGCCGTCGTCCAAATCCTCATGCTAAACCACTGCACTT 335
 Db 685 TACCTCAGACATCAACCTGGGACGTCGTGGAATCCTCATGCCAAACCACTGCACTT 744
 Qy 336 TCACCTCTTGAAGTATCGGAAGGCGAGTTTGGAAAGGTTCTTACGACAGACAAA 395
 Db 745 TGATTTCTTAAAGTTATTGGAAGGCGAGTTTGGCAAGGTTCTTCTTCAAAAACGGA 804
 Qy 396 GGCAGAGAGAGTGTCTTATCAGTCAAAAGTTTACAGAAAGCAATCCTGAAAGAA 455
 Db 805 ACTGGATGGAATTTTATGCTGTCAAGTGTACAGAAAAAATAGTTCTCAACAGAA 864
 Qy 456 AGAGGAGAACATATTATGTGCGAGCGGAATGTTCTGTGTAAGAATGTGAAGCACCTTT 515

Db 865 AGAGCAAAACATATTATGGCTGAACGTAATGTGCTCTTGA AAAATGTGAACATCCGTT 924
 Qy 516 CTTGGTGGGCTTCACTTCTCTTCCAGACTGCTGACAAATGTACTTTGTCTCTAGACTA 575
 Db 925 TTTGGTGGATTCATATTCTTCCAAACAACCTGAAAGCTTTATTTTGTCTGATTT 984
 Qy 576 CATTAATGGTGGAGAGTTGTTCTTACCATCTCCAGAGGGAACGCTGCTTCTGTGAACACG 635
 Db 985 TGGTTATGAGGGGAGCTTTTTCACATTACAAAGAGAACGCTCTCTTCTGAGCACAG 1044
 Qy 636 GGCTCGTTTCTATGCTGCTGAAATAGCCAGTGGCTTGGGCTACCTGCATCTCACTGAACAT 695
 Db 1045 AGCTAGTGTTCAGCTGCTGAAATTTGCTAGTGCATTTGGGTTACTTACATTTCCATCAAAT 1104
 Qy 696 CGTTTATAGAGACTTAAACACAGAGAAATATTTTGTAGATTTCACAGGGACACATTTGCTCT 755
 Db 1105 AGTATACAGAGACTTGAACACAGAAATATCTTTTGGATTTCAGTAGGACATGTTGTCTT 1164
 Qy 756 TACTGACTTCGGACTCTGCAAGGAGAAACATTGAAACACACAGCACAAACATCCACCTTTCTG 815
 Db 1165 AACAGATTTTGGGCTTTGTAAGAGAGGAATTTGCTATTTCTGACACCACTACACATTTTG 1224
 Qy 816 TGGCAGCCGGAGTATCTCGACCTGAGTGTCTTATAAGCAGCCTTTATGACAGGACTGT 875
 Db 1225 TGGGACACAGAGATATCTTGCACCTGAGTAATTAGAAAAACAGCCCTATGACAATACTGT 1284
 Qy 876 GGACTGGTGGTGGGAGCTGTCTTGTATGAGATGCTGTATGGGCTCGCGCTCTTTTA 935
 Db 1285 AGATTGGTGGTGGGCTGTCTGTATGAAATGCTGTATGGAATGCTGCTCTCTTTTA 1344
 Qy 936 TAGCCGAAACACAGCTGAAATGTACCAACAACTTCTGAAACAAAGCCTCTCCAGCTGAAACC 995
 Db 1345 TTGCCGAGATGTTGCTGAAATGTATGACAAATATCTTTCACAAACCCCTAAGTTTGAGGCC 1404
 Qy 996 AAATATTACAAATTCGCAAGACACCTCTCGAGGGCCCTCTGCAAGAGACAGGACAAA 1055
 Db 1405 AGGAGTGAGTCTTACAGCCTGGTCCATTCTGGAAGAACTCTTAGAAAAAGACAGGCAAAA 1464
 Qy 1056 GGGCTCGGGCCAGGATGACTTCATGAGATTAAGACTGATGTTCTTCTCTCTTAAT 1115
 Db 1465 TGACTTGGTGCCAGGAGAGACTTCTTGAATTCAGAATCATCTTTTGTGAATCACT 1524
 Qy 1116 TAACTGGGATGATCTCATTAATAAGAGATTAATCTCCCTCTTAAACCAAAATGTGAGTGG 1175
 Db 1525 CAGCTGGGCTGACCTTGTACAAAAGAGATTCCACACCACTTAATCTTAATGTGCTGG 1584
 Qy 1176 GCCCAACGACCTACGCACTTTTGACCCCGAGTTTACGAGAGCCTGTGCCCCAATCCAT 1235
 Db 1585 ACCAGATGATATCAGAAACTTTGACACAGCAATTTACAGAAAGAAACAGTTCCATATTCTGT 1644
 Qy 1236 TGGCAAGTCCCTGACAGCGTCTCTGTCACAGCCAGGCTCAAGGAGCTGCCGAGGCTTT 1295
 Db 1645 GTGTGTATCTTCTGACTATTTCTATAGTGAATGCCAGTGTATTGGAGGCGAGATGATGAT 1704
 Qy 1296 CTTAGGCTTTTCTCTATGCGCTCCCAACGGA 1325
 Db 1705 CGTTGGTTTCTCTATGCACTCTCTTCAGA 1734

RESULT 10

US-09-925-300-860
 ; Sequence 860, Application US/09925300
 ; Patent No. US20020151681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; APPLICANT: Steve Ruben,
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA101
 ; CURRENT APPLICATION NUMBER: US/09/925,300
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05988
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270

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; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 860
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (379)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (401)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-860

Query Match      30.7%; Score 410.4; DB 10; Length 423;
Best Local Similarity 97.9%; Pred. No. 4.7e-122;
Matches 414; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 671 TGGGCTACCTGCATTCACTCAACATCGTTTATAGAGACTTAAACACAGAGAAATTTTGC 730
Db 1 TGGGCTACCTGCATTCACTCAACATCGTTTATAGAGACTTAAACACAGAGAAATTTTGC 60

QY 731 TAGATTACAGAGGACACATTTGCTTACTGACTTCGGACTCTGCAAGGAGAAACATTGAAC 790
Db 61 TAGATTACAGAGGACACATTTGCTTACTGACTTCGGACTCTGCAAGGAGAAACATTGAAC 120

QY 791 ACAACAGCAACATCCACCTTCTGTGGCACGCGGAGTATCTCGCACCTTGAGGTCTTC 850
Db 121 ACAACAGCAACATCCACCTTCTGTGGCACGCGGAGTATCTCGCACCTTGAGGTCTTC 180

QY 851 ATAAGCAGCTTATGACAGACTGTGACCTGTGTGGTCTTGGAGCTTCTTGTATGAGA 910
Db 181 ATAAGCAGCTTATGACAGACTGTGACCTGTGTGGTCTTGGAGCTTCTTGTATGAGA 240

QY 911 TGTGTATGCTTGGCTGCGCCCTTTTATAGCCGAAACACAGCTGAAATGTAGCAACATTC 970
Db 241 TGTGTATGCTTGGCTGCGCCCTTTTATAGCCGAAACACAGCTGAAATGTAGCAACATTC 300

QY 971 TGAACAGCTCTCCAGCTGAACCAATATTACAAATTCGCAAGACACCTCTCTGGAGG 1030
Db 301 TGAACAGCTCTCCAGCTGAACCAATATTACCAATTCGCAAGACACCTCTCTGGAGG 360

QY 1031 GCTCTCTGCAAGGACAGCAACAGCGCTCGGGCCAGGATGACTTTCATGGAGTTA 1090
Db 361 GCTCTCTGNAAGAGGACANCAAGCGCTCGGGCCAGGATGACTTTCATGGAGTTA 420

QY 1091 AGA 1093
Db 421 AGA 423

RESULT 11
US-09-918-995-15481
; Sequence 15481, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15481
; LENGTH: 447

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1)_(447)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-15481

Query Match      28.7%; Score 383.4; DB 9; Length 447;
Best Local Similarity 97.7%; Pred. No. 2.7e-113;
Matches 387; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 943 AACACAGCTGAATGTACGACAAACATCTGAAACAAGCCTCTCCAGCTGAACCAATATT 1002
Db 32 ATCCCAGCNGACANGNACGACAAACATCTGAAACAAGCCTCTCCAGCTGAACCAATATT 91

QY 1003 ACAAAATTCGCAAGACACACCTCTCGGAGGCGCTCTCGAAGGACAGGACAAAGCGCTC 1062
Db 92 ATTAATTCGCAAGACATCTCTCGGAGGCGCTCTCGAAGGACAGGACAAAGCGCTC 151

QY 1063 GGGGCCAAGGATGACTTTCATGGAGATTAAGAGTCATGTCTTCTCTCTTAATTAAGTGG 1122
Db 152 GGGGCCAAGGATGACTTTCATGGAGATTAAGAGTCATGTCTTCTCTCTTAATTAAGTGG 211

QY 1123 GATGATCTCATTAATTAAGAGATTAATCTCCCTCTTTTAAACCAATGTAGTGGGCCAAC 1182
Db 212 GATGATCTCATTAATTAAGAGATTAATCTCCCTCTTTTAAACCAATGTAGTGGGCCAAC 271

QY 1183 GACCTACGCGACTTTTCACCCCGAGTTTACCGAGAGCGCTCTCCCACTTCATTGGCAAG 1242
Db 272 GACCTACGCGACTTTTACCCCGAGTTTACCGAGAGCGCTCTCCCACTTCATTGGCAAG 331

QY 1243 TCCCTCTGACAGCGCTCTCTGTCACAGCAGCGTCAAGGAAAGCTCCCGAGGCTTTCTTAGGC 1302
Db 332 TCCCTCTGACAGCGCTCTCTGTCACAGCAGCGTCAAGGAAAGCTCCCGAGGCTTTCTTAGGC 1302

QY 1303 TTTTCTATGCGCTCTCCAGGACTCTTTCTCTGA 1338
Db 392 TTTTCTATGCGCTCTCCAGGACTCTTTCTCTGA 427

RESULT 12
US-09-764-868-56
; Sequence 56, Application US/09764868
; Patent No. US2002016871A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 851
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (51)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (846)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-56

Query Match      26.3%; Score 351.6; DB 9; Length 851;
Best Local Similarity 66.6%; Pred. No. 8e-103;
Matches 498; Conservative 3; Mismatches 247; Indels 0; Gaps 0;
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Qy 1206 GTTACCAGAGAGCTCTCCCACTCCATTCGAGTCCCTGACAGGCTCTCTGTAC 1265
Db 192 GTTCACTGAAGAGCGGTCCCACTCCATTCGAGTCCCTGACAGGCTCTCTGTAC 251
Qy 1266 AGCCAGGCTCAAGAGAGCTCCGAGGCTTTCCTAGGCTTTTCTATCGGCTCCACGGA 1325
Db 252 AGCCAGGCTCAAGAGAGCGGTGAGGCTTCTCTGGGCTTTTCTATGACCTCCATGGA 311
Qy 1326 CTCTTCTCTCTGA 1338
Db 312 CTCTTCTCTCTGA 324

RESULT 15

US-09-918-995-10666
; Sequence 10666, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10666
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(557)
; OTHER INFORMATION: n = A, T, C or G
US-09-918-995-10666

Query Match 19.5%; Score 260.8; DB 9; Length 557;
Best Local Similarity 69.6%; Pred. No. 1.4e-73;
Matches 352; Conservative 0; Mismatches 154; Indels 0; Gaps 0;
Qy 340 TTCTTGAAGTATCGAAGAGGCGAGTTTGGAAAGTCTCTTAGCAAGACACAGGCA 399
Db 50 TTCTTAAAGTTATTGGAAGAGGCGAGTTTGGCAAGTCTCTTGCAGAAACGAAACTG 109
Qy 400 GAAGAGCTGTCTATGACGTCAGTCAAGTTTACAGAGAGAGCAATCTCGAAAGAGAGAG 459
Db 110 GATGGAAATTTTATGCTGTCAGAGTGTACAGAAAAAATAGTTCTCAACAGAAAAAGAG 169
Qy 460 GAGAAGCATATTATGTCGAGCGGAATGTTCTGTGAAGATGTGAAGCACCTTTTCCTG 519
Db 170 CAAAAACATATTATGGCTGAACGTATGTGCTCTTGAAGAAATGTGAACATCCGTTTTG 229
Qy 520 GTGGCCCTTCACTTCTCTTTCAGACGTGCTGACAAATTTGTACTTTGTCTAGACTACATT 579
Db 230 GTTGGATTGCAATTATCTCTTCCAAACAACTGAAAGCTTTATTTTGTCTGGATTTGTT 289
Qy 580 AATGGTGGAGAGTTGTTCTACCATCTCCAGAGGGAAGCTTCTCTGGAAACACCGGCT 639
Db 290 AATGGAGGGGAGCTTTTTCACCTTACAAAGAGAGACGGTCTTCTCTGAGACAGAGCT 349
Qy 640 CGTTTCTATGCTGTAATAGCAGTGCCTTGGGCTACCTGCAATTCACCTGAACATCGTT 699
Db 350 AGGTTTACCGTCTGAAATTTGCTAGTGCATTGGGTTACTTACATTCCTCAAAANTAGTA 409
Qy 700 TATAGACATTAAACCAGAGATATTTTCTAGATTTCACAGGACACATTTGCTTACT 759
Db 410 TACAGAGACTTGAACCAGAAATATTTCTTTTGGATTTCAGTAGACATGTTGCTTAAACA 469
Qy 760 GACTTCGAGCTCTCAGAGAGACATTTGAACACACAGACACACATCCACCTTCTGTGGC 819
Db 470 GATTTTNGCTTTGTAAAGAAGGAATTTGCTATTTCTGACACCACTACCACTTTGTGGG 529

Qy 820 ACGCCGAGTATCTCGACCTGAGGT 845
Db 530 ACACCAGAGATCTTGCACCTGAAGT 555
Search completed: June 25, 2003, 10:34:30
Job time : 165 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1219.8	91.2	2311	2	US-08-712-709-6	Sequence 6, Appli
2	1219.8	91.2	2311	3	US-09-111-444-6	Sequence 6, Appli
3	1219.8	91.2	2311	4	US-09-541-228-6	Sequence 6, Appli
4	1218.2	91.0	2370	4	US-09-031-295-1	Sequence 1, Appli
5	255.2	19.1	2610	2	US-09-212-771-1	Sequence 1, Appli
6	255.2	19.1	2610	3	US-09-091-058-1	Sequence 1, Appli
7	248.4	18.6	1599	3	US-09-256-465-1	Sequence 1, Appli
8	248.4	18.6	1399	4	US-09-167-323-3	Sequence 3, Appli
9	241	18.0	2245	4	US-09-225-749-24	Sequence 24, Appli
10	235.4	17.6	2599	6	5266464-1	Patent No. 5266464
11	230.8	17.2	2104	3	US-09-313-930-1	Sequence 1, Appli
12	230.6	17.2	2244	3	US-09-094-714A-48	Sequence 48, Appli
13	214.6	16.0	2754	4	US-09-429-322-3	Sequence 3, Appli
14	200.2	15.0	1732	4	US-09-430-564-1	Sequence 1, Appli
15	185.6	13.9	266	1	US-08-594-031-164	Sequence 164, Appli
16	183.4	13.7	2549	4	US-09-467-082-3	Sequence 3, Appli
17	179.2	13.4	1637	2	US-08-966-316-10	Sequence 10, Appli
18	176.6	13.2	2196	1	US-08-313-274-1	Sequence 1, Appli
19	136.6	10.2	1890	3	US-09-289-466-2	Sequence 2, Appli
20	135	10.1	1891	3	US-09-289-466-1	Sequence 1, Appli
21	135	10.1	1929	2	US-09-016-000-10	Sequence 10, Appli
22	127.6	9.5	1276	1	US-07-688-352C-25	Sequence 25, Appli
23	127.6	9.5	1276	5	PCR-US91-02714-24	Sequence 24, Appli
24	122.2	9.1	688	4	US-08-998-416-90	Sequence 90, Appli
25	121.2	9.1	1273	2	US-08-474-379C-25	Sequence 25, Appli
26	121.2	9.1	1273	3	US-09-146-249A-25	Sequence 25, Appli
27	121.2	9.1	1273	3	US-08-206-189B-25	Sequence 25, Appli

Db 83 TCCTTTTCATGAAGCAGGAGGATGGTCTGAACGACTTTATTTCAGAAGATTGCCAATA 142
Qy 176 ACTCCTATGATGCAACACCCCTGAGTTTCAGTCCATCTTTGAAGATCTCCCAACCTCAGG 235
Db 143 ACTCCTATGATGCAACACCCCTGAGTTTCAGTCCATCTTTGAAGATCTCCCAACCTCAGG 202
Qy 236 AGCTGAGCTTATGATGCAACCCCTTCTCCTCCACCAAGTCTCTCTCAGCAAAATCAACC 295
Db 203 AGCTGAGCTTATGATGCAACCCCTTCTCCTCCACCAAGTCTCTCTCAGCAAAATCAACC 262
Qy 296 TTGGCCCGTCCGTCATCTGCTAAACCATCTGACTTTTCACTCTTTGAAAGTATCG 355
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Qy 356 GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAGACACAGGCGAGAAGTCTTCTATG 415
Db 323 GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAGACACAGGCGAGAAGTCTTCTATG 382
Qy 416 CAGTCAAAAGTTTACAGAAGAAAGCAATCTGTAAGAAAGAAAGAGGAGCAATATTATGT 475
Db 383 CAGTCAAAAGTTTACAGAAGAAAGCAATCTGTAAGAAAGAAAGAGGAGCAATATTATGT 442
Qy 476 CGAGCGGAATGTTCTGTTGAAGAAATGTAAGCAACCTTTCTGGTGGGCTTCACTTCT 535
Db 443 CGAGCGGAATGTTCTGTTGAAGAAATGTAAGCAACCTTTCTGGTGGGCTTCACTTCT 502
Qy 536 CTTTCCAGACTGCTGCAAAATGTAATTTGTTCTCTAGACTACATTAATGGTGGAGATTGT 595
Db 503 CTTTCCAGACTGCTGCAAAATGTAATTTGTTCTCTAGACTACATTAATGGTGGAGATTGT 562
Qy 596 TCTACCATCTCCAGAGGGAACGCTGCTCTGGAACCAACCGGCTCGTTTCTATGCTGCTG 655
Db 563 TCTACCATCTCCAGAGGGAACGCTGCTCTGGAACCAACCGGCTCGTTTCTATGCTGCTG 622
Qy 656 AAATAGCAGTCTGGGCTGCTGCTGCAATCTGCAATCTGCAATCTGTTATAGAGACTTAAAC 715
Db 623 AAATAGCAGTCTGGGCTGCTGCTGCAATCTGCAATCTGTTATAGAGACTTAAAC 682
Qy 716 CAGAGATATTTGCTAGATTACAGGGAACATTTGCTTCTTACTGACTTCGGACTCTGCA 775
Db 683 CAGAGATATTTGCTAGATTACAGGGAACATTTGCTTCTTACTGACTTCGGACTCTGCA 742
Qy 776 AGAGAAATTTGAACACACAGACACATCTGCTGGCAGCCCGGAGTATCTCG 835
Db 743 AGAGAAATTTGAACACACAGACACATCTGCTGGCAGCCCGGAGTATCTCG 802
Qy 836 CACTGAGTCTTTATAGCAGCCTTATGACAGGACTGTGGAAGTGGTGGCTGGGAG 895
Db 803 CACTGAGTCTTTATAGCAGCCTTATGACAGGACTGTGGAAGTGGTGGCTGGGAG 862
Qy 896 CTGCTTGTATGAGATCTGTATGGCTGCGGCTTTTATAGCCGAAACACAGCTGAAA 955
Db 863 CTGCTTGTATGAGATCTGTATGGCTGCGGCTTTTATAGCCGAAACACAGCTGAAA 922
Qy 956 TGTACGACAAATCTGAAACAGCTCTCAGCTGAAACCAATATTACAAATTCGCA 1015
Db 923 TGTACGACAAATCTGAAACAGCTCTCAGCTGAAACCAATATTACAAATTCGCA 982
Qy 1016 GACACTCTCTGGAGGCTCTCTGAGAGACAGGACAAACGCGCTGGGGCCAAAGATG 1075
Db 983 GACACTCTCTGGAGGCTCTCTGAGAGACAGGACAAACGCGCTGGGGCCAAAGATG 1042
Qy 1076 ACTTCATGGAGATTAGAGTCAATGCTTCTTCTTCTTAACTGGATGATCTCATTA 1135
Db 1043 ACTTCATGGAGATTAGAGTCAATGCTTCTTCTTCTTAACTGGATGATCTCATTA 1102
Qy 1136 ATAAGAGATTACTCCCTCTTTAAACCAATATGAGTGGGCCCCAACGACTACGGCACT 1195
Db 1103 ATAAGAGATTACTCCCTCTTTAAACCAATATGAGTGGGCCCCAACGACTACGGCACT 1162
Qy 1196 TTGACCCGAGTTTACGAGAGCCTGTGCTCCCAACTCTCATTTGGCAAGTCCCTTGACAGCG 1255
Db 1163 TTGACCCGAGTTTACGAGAGCCTGTGCTCCCAACTCTCATTTGGCAAGTCCCTTGACAGCG 1222

Qy 1256 TCCTGTCACAGCCAGCGTCAAGGAGCTGCCAGGCTTTCTTAGGCTTTTCTATGCGC 1315
Db 1223 TCCTGTCACAGCCAGCGTCAAGGAGCTGCCAGGCTTTCTTAGGCTTTTCTATGCGC 1282
Qy 1316 CTCCACCGGACTCTTTCTCTCTGA 1338
Db 1283 CTCCACCGGACTCTTTCTCTCTGA 1305

RESULT 2

US-09-111-444-6
; Sequence 6, Application US/09111444
; Patent No. 6045792
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,444
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-09-111-444-6

Query Match 91.2%; Score 1219.8; DB 3; Length 2311;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 116 TGGCTTTTCATGAAGCAGGAGGATGGTCTGAACGACTTTATTTCAGAAGATTGCCAATA 175
Db 83 TGGCTTTTCATGAAGCAGGAGGATGGTCTGAACGACTTTATTTCAGAAGATTGCCAATA 142
Qy 176 ACTCCTATGATGCAACACCCCTGAGTTTCAGTCCATCTTTGAAGATCTCCCAACCTCAGG 235
Db 143 ACTCCTATGATGCAACACCCCTGAGTTTCAGTCCATCTTTGAAGATCTCCCAACCTCAGG 202
Qy 236 AGCTGAGCTTATGATGCAACCCCTTCTCCTCCACCAAGTCTCTCTCAGCAAAATCAACC 295
Db 203 AGCTGAGCTTATGATGCAACCCCTTCTCCTCCACCAAGTCTCTCTCAGCAAAATCAACC 262

QY 296 TTGSCCGTCTGCTCAATCTCATGCTAAACCATCTGACTTTCACCTTCTGAAAGTGATCG 355
Db 263 TTGSCCGTCTGCTCAATCTCATGCTAAACCATCTGACTTTCACCTTCTGAAAGTGATCG 322
QY 356 GAAAGGCGAGTTTGGAAAGTCTCTAGCAAGACACAAAGGCAAGAGAGAGTGTCTATG 415
Db 323 GAAAGGCGAGTTTGGAAAGTCTCTAGCAAGACACAAAGGCAAGAGAGTGTCTATG 382
QY 416 CAGTCAAGTTTACAGAGAGCAATCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 475
Db 383 CAGTCAAGTTTACAGAGAGCAATCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 442
QY 476 CGAGCGGAGATGTTCTGAG 535
Db 443 CGAGCGGAGATGTTCTGAG 502
QY 536 CTTTCCAGACTGCTGACAAATTTGACTTTTGTCTAGACTACATTAATGTTGGAGAGTTGT 595
Db 503 CTTTCCAGACTGCTGACAAATTTGACTTTTGTCTAGACTACATTAATGTTGGAGAGTTGT 562
QY 596 TCTACCATCTCCAGAGGAG 655
Db 563 TCTACCATCTCCAGAGGAG 622
QY 656 AATAGCAGCTGCTGGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 715
Db 623 AATAGCAGCTGCTGGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 682
QY 716 CAGAGAAATTTTGTAGATTTACAGGAGACACATTTGCTTACTGACTTCGGACTCTGCA 775
Db 683 CAGAGAAATTTTGTAGATTTACAGGAGACACATTTGCTTACTGACTTCGGACTCTGCA 742
QY 776 AGAGAAATTTTGTAGATTTACAGGAGACACATTTGCTTACTGACTTCGGACTCTGCA 835
Db 743 AGAGAAATTTTGTAGATTTACAGGAGACACATTTGCTTACTGACTTCGGACTCTGCA 802
QY 836 CACTGAGGCTTTCATAG 895
Db 803 CACTGAGGCTTTCATAG 862
QY 896 CTGCTTGTATGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 955
Db 863 CTGCTTGTATGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 922
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Db 923 TGTAAGCAAAATTTGAAAG 982
QY 1016 GACACTCTCTGGAGGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1075
Db 983 GACACTCTCTGGAGGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1042
QY 1076 ACTTCAGGAGATTAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1135
Db 1043 ACTTCAGGAGATTAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1102
QY 1136 ATAAGAGATTAATCTCCCTCTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1195
Db 1103 ATAAGAGATTAATCTCCCTCTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1162
QY 1196 TTGACCCGAGTTTACGAG 1255
Db 1163 TTGACCCGAGTTTACGAG 1222
QY 1256 TCCTGTCAG 1315
Db 1223 TCCTGTCAG 1282
QY 1316 CTCCACGAGACTCTTCTCTCTGA 1338
Db 1283 CTCCACGAGACTCTTCTCTCTGA 1305

RESULT 3
US-09-541-228-6
; Sequence 6, Application US/09541228
; Patent No. 6232077
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/541,228
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
; US-09-541-228-6
Query Match 91.2%; Score 1219.8; DB 4; Length 2311;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 116 TGGCTTTTCATGAAGCAG 175
Db 83 TGGCTTTTCATGAAGCAG 142
QY 176 ACTCTATGATGCAACCAACCCCTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235
Db 143 ACTCTATGATGCAACCAACCCCTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 202
QY 236 AGCTGAGCTTATGAATGCAACCCCTTCCTCCACCAAGTCTCTCAGCAAACTCAAC 295
Db 203 AGCTGAGCTTATGAATGCAACCCCTTCCTCCACCAAGTCTCTCAGCAAACTCAAC 262
QY 296 TTGGCCCGTCGTCCTCAATCTGCTTAAACCATCTGACTTTCACCTTCTTGAAGTGTATG 355
Db 263 TTGGCCCGTCGTCCTCAATCTGCTTAAACCATCTGACTTTCACCTTCTTGAAGTGTATG 322
QY 356 GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAGACACAAAGGCAAGAGAGAGAGAGAGAG 415
Db 323 GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAGACACAAAGGCAAGAGAGAGAGAGAGAG 382
QY 416 CAGTCAAGTTTACAGAGAGCAATCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 475

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Db 383 CAGTCAAGATTTTACAGAGAAAGCAATCCTGAAAAAGAGAGAGCAATATTATGT 442
Qy 476 CGGAGCGGAATGTTCTGTGAAGAAATGTAAGACACCTTTCTGTGGGCTTCACTTCT 535
Db 443 CGGAGCGGAATGTTCTGTGAAGAAATGTAAGACACCTTTCTGTGGGCTTCACTTCT 502
Qy 536 CTTTCCAGACTGCTGACAAATTTGACTTTTGTCTAGACTACATTAATGTTGGAGAGTTGT 595
Db 503 CTTTCCAGACTGCTGACAAATTTGACTTTTGTCTAGACTACATTAATGTTGGAGAGTTGT 562
Qy 596 TCTACCATCTCCAGAGGAACGCTGCTTCTGGAACCAACGCGGCTGTTTCTATGCTGCTG 655
Db 563 TCTACCATCTCCAGAGGAACGCTGCTTCTGGAACCAACGCGGCTGTTTCTATGCTGCTG 622
Qy 656 AATAGCAGCTGCTTGGGCTACTGCTGATTCACCTGACATCGTTTATAGAGACTTAAAC 715
Db 623 AATAGCAGCTGCTTGGGCTACTGCTGATTCACCTGACATCGTTTATAGAGACTTAAAC 682
Qy 716 CAGAGAAATATTTGCTAGATTTCAGGGGACACATTTGCTTACTGACTTCGGACTCTGCA 775
Db 683 CAGAGAAATATTTGCTAGATTTCAGGGGACACATTTGCTTACTGACTTCGGACTCTGCA 742
Qy 776 AGGAGAAATGTAACACAGACACAAATCCACCTTTCTGTGGACGCCGGAGTATCTCG 835
Db 743 AGGAGAAATGTAACACAGACACAAATCCACCTTTCTGTGGACGCCGGAGTATCTCG 802
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Db 803 CACTGAGGCTTCTAAGCAGCTTATGACAGGACTGTTGACTGTTGGTCTGCTGGAG 862
Qy 896 CTGTCTTGTATGAGATCTGTATGGCTGCGCTTTTATAGCCGAAAAACAGCTGAAA 955
Db 863 CTGTCTTGTATGAGATCTGTATGGCTGCGCTTTTATAGCCGAAAAACAGCTGAAA 922
Qy 956 TGTACGACAACTTCTGAAACAGCTCTCCAGCTGAAACCAAAATATTACAAATTCGCA 1015
Db 923 TGTACGACAACTTCTGAAACAGCTCTCCAGCTGAAACCAAAATATTACAAATTCGCA 982
Qy 1016 GACACTCTCTGGAGGCTCTCTGAGAGGACGAGCAAGCGCTCGGGCCAGAGTG 1075
Db 983 GACACTCTCTGGAGGCTCTCTGAGAGGACGAGCAAGCGCTCGGGCCAGAGTG 1042
Qy 1076 ACTTCATGAGATTAAGAGTCATGCTTCTTCTTAAATTAAGTGGATGATCTCATTA 1135
Db 1043 ACTTCATGAGATTAAGAGTCATGCTTCTTCTTAAATTAAGTGGATGATCTCATTA 1102
Qy 1136 ATAAGAAATTAATCTCCCTTTTAAACCAAAATGTAAGTGGGCCCCAAGCTACGGCACT 1195
Db 1103 ATAAGAAATTAATCTCCCTTTTAAACCAAAATGTAAGTGGGCCCCAAGCTACGGCACT 1162
Qy 1196 TTGACCCCGAGTTTACCGAGAGCTGCTCCCACTCCATTTGGCAAGTCCCTGACAGCG 1255
Db 1163 TTGACCCCGAGTTTACCGAGAGCTGCTCCCACTCCATTTGGCAAGTCCCTGACAGCG 1222
Qy 1256 TCCTCGTCACAGCAGCGCTCAAGGAAGCTGCGGAGGCTTTCTAGGCTTTTCTATGCGC 1315
Db 1223 TCCTCGTCACAGCAGCGCTCAAGGAAGCTGCGGAGGCTTTCTAGGCTTTTCTATGCGC 1282
Qy 1316 CTCCACGGACTCTTCTCTGTA 1338
Db 1283 CTCCACGGACTCTTCTCTGTA 1305

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RESULT 4

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US-09-031-295-1
; Sequence 1, Application US/09031295
; Patent No. 6326181
; GENERAL INFORMATION:
; APPLICANT: LANG, Florian
; APPLICANT: WALDEGER, Tubingen
; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,295
; FILING DATE: 26-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 197-08-173.8
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 058315/0123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2370 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1335
; US-09-031-295-1

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Query Match 91.0%; Score 1218.2; DB 4; Length 2370;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 116 TGGCTTTTCATGAGCAGAGAGGAGTGGGTCTGAACGACCTTTATTCAGAAGATTGCCAATA 175
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Qy 536 CTTTCCAGACTGCTGCAAAATTTGACTTTTGTCTAGACTACATTAATGTTGGAGAGTTGT 595
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Db 716 CAGAGAATATTTTGTCTAGATTCACAGGACACATTTGTCCTTACTGACTTCGGACTCTGCA 775
QY 776 AGAGAAATTTGAACACAGACACATCTCTGCTGCAACCGCGGAGTATCTCG 835
Db 776 AGAGAAATTTGAACACAGACACATCTCTGCTGCAACCGCGGAGTATCTCG 835
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Db 836 CACTGAGGTGCTTCTAAGCAGCTTATCAGAGGACTGTGGACTGTGGTGTCTGGAG 895
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Db 896 CTGTCTTTGTATGAGATGCTGTATGGCTGCGCTTTTATAGCCGAAACACAGCTGAAA 955
QY 956 TGTACGACAACTTCTGAACAGCTCTCCAGCTGAAACCAATATTAATAATTCGCA 1015
Db 956 TGTACGACAACTTCTGAACAGCTCTCCAGCTGAAACCAATATTAATAATTCGCA 1015
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Db 1016 GACACTCTCTGGAGGCTCTCCAGAGGACAGGACAAAGCGCTCGGGCCCAAGGATG 1075
QY 1076 ACTTCATGAGATTAAGAGTCACTGTCTTCTTCTTAACTTAACTGGGATGATCTCATTA 1135
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QY 1136 ATAAGAAATTAATCTCCCTTTTAAACCAATGTAGTGGGCGGCAACGACTACGGCACT 1195
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QY 1316 CTCCACGAGCTCTTCTCTGA 1338
Db 1316 CTCCACGAGCTCTTCTCTGA 1338

RESULT 5

US-09-212-771-1
; Sequence 1, Application US/09212771
; Patent No. 5958773
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212,771
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-212-771-1

Query Match 19.1%; Score 255.2; DB 2; Length 2610;
Best Local Similarity 57.4%; Pred. No. 7e-72;
Matches 521; Conservative 0; Mismatches 378; Indels 9; Gaps 3;
QY 331 GACTTTCACTTCTTGAAGTGATCGAAAGGGCAGTTTGGAAAGGTTCTTCTAGCAAGA 390
Db 643 GAGTTTGTAGTACTGAAGCTGTGGCAAGGGCAGTTTCTGGCAAGTGATCTCTGGTGAAG 702
QY 391 CACAAGGCAAGAAAGTGTCTATGCACTCAAGTTTACAGAAAGAAAGCAATCTCTGAAA 450
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QY 511 CCTTCTCTGGTGGGCTTCACTTCTCTTTCAGAGCTGTGACAAATGTACTTTGTCTTA 570
Db 820 CCTTCTCTCACAGCCCTGAAGTACTCTTTCAGACCCACGACGCGCTCTGCTTTGTCTATG 879
QY 571 GACTACATTAATGGTGGAGAGTTGTTTACCATCTCCAGAGGGAAGCGCTCTCTCTGGAA 630
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Db 1120 ACCTTTTGGGCACACCTGAGTACCTGGCCCCCGAGGTCTGGAGGACAATGACTACGGC 1179
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QY 928 CTTTTTATAGCGGAACACAGCTGAATGTAGCAACATCTCTGAACAGCTCTCTCCAG 987
Db 1240 CCCTTCTCAACAGAGCCATGAGAAAGCTTTTGAAGCTCATCTCTATGAGGAGATCCGC 1299
QY 988 CTGAACACCAATATTAACAAATCCGCAAGACACCTCTCTGGAGGGCTCTCTGCAAGAGGAC 1047
Db 1300 TTTCCCGCGCAGCTTGGTCCCGAGGCCAAGTCTTCTGCTTTCAGGGCTGTCTCAAGAGGAC 1359
QY 1048 AGGACAAAGCGGCT---CGGGCCAAAGATGACTTTCATGGAGATTAAAGATGATGCTTC 1104
Db 1360 CCAAGCAGAGGCTTGGCGGGGCTCCGAGGACGCCAAGAGGAGATCATGACGATCGCTTC 1419
QY 1105 TTCTCCTTAATTAATCGGGATGATCTCATTAATAAGAGATTAATCCCCCTTTTAAACCCA 1164
Db 1420 TTGCGGCTATCGTGTGGCAGCACGTGTACGAGAAAGAGCTACGCCCAACCTTCAAGCCC 1479
QY 1165 AATGTAGTGGGCCCCAACACCTACCGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTC 1224
Db 1480 CAGGTACGTCGAGACTGACACAGGTATTTTGTAGAGAGTTTACGCGCCAGATGATC 1539
QY 1225 CCAACTC 1232
Db 1540 ACCATCAC 1547

RESULT 6

US-09-091-058-1
; Sequence 1, Application US/09091058

```

; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A.
; APPLICANT: Frech, Matthias
; TITLE OF INVENTION: Screening Method
; FILE REFERENCE: 4-20583/A/20684/PCT
; CURRENT APPLICATION NUMBER: US/09/091,058
; CURRENT FILING DATE: 1998-06-10
; EARLIER APPLICATION NUMBER: PCT/EP96/04814
; EARLIER FILING DATE: 1996-11-05
; EARLIER APPLICATION NUMBER: 9525703.6
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-091-058-1

Query Match          19.1%; Score 255.2; DB 3; Length 2610;
Best Local Similarity 57.4%; Pred. No. 7e-72;
Matches 521; Conservative 0; Mismatches 378; Indels. 9; Gaps 3;

QY      331  GAC TTT CAC TTT CTT GAA AGT GAT CGG AAG GGG CAG TTT TCG AAA AG GTT TCT TCT TAG CAA GA 390
DB      643  GAG TTT GAG TAC CTG AAG CTG CTG GGC AAG GGG CAC TTT TCG CAA AG GTG ATC TCT GTG TGA G 702
QY      391  CACA AGG CAGA AAG AGT GTT C TAT GCA GT CAA AG TTTT TAC AGA AAG AAG CAAT CCT GAAA 450
DB      703  GAGA AGG CAC AGG CGC TACT ACG CCA TGA AG ATC TCA AGA AGA AGT CAT CGT GGC 762
QY      451  AAGA AGA GAG AAG CATA TAT TAT GTC GAG GGG AAT GTT C TGT TGA AAT GTG AAG CAC 510
DB      763  AAGG AC GAG GTG GGC CCA CAC ACT CAC CGA --- GAA CGG CGT C TCT G CAG AACT C CAGG CAC 819
QY      511  CCT TTT CCG TGT GGG CCT TCA CTT C TCT TTT CC AGA CTG CTG ACAA AT TGT ACT TTT GT CCA 570
DB      820  CCT TTT CCA GCC CTG AAG TACT C TTT TCA GAC CCA CAG CCG C TCT GCT TTT GT CATG 879
QY      571  GACT ACA TTA ATG GTG AGA GTT TGT TCT ACC ATCTCC AGA GGG AAG C GCT GCT TCT TGG AA 630
DB      880  GAGTAC GCC AAC GGG GCG AGC TGT TCT TCC ACC TGT CCG GGA ACG GTG TGT TCT CCG AG 939
QY      631  CCA CGG C TCG TTT CTA TGT C TGT GAA ATG CCA AGT G C C TTT GGG C TAC C TGT C A T C --- A 687
DB      940  GAC CGG CCG C C T TCT ATG GCG CTG AGA TGT GTG CAG CCG C TGT GGA C TAC C TGT C A C TCG GAG 999
QY      688  CTG ACA T C C T TAT AGA GACT TTA AACC AGA AATAT TTT TGT AGA TTT CAC AGG GAC AC 747
DB      1000  AAGA AC TGT GTG TAC CCG GAC C C TCA A C TGT GGA AACT C A T G C TGT GGA AAG GAG GCG CAC 1059
QY      748  ATT GTC C T TACT GACT TTT CGG A C TCTG CAA AGG AAG AACA T TGA ACA CAC AG CACA A C TCC 807
DB      1060  ATTA AG ATC A CAG ACT TCG G C TGTG CAA GAG GGG ATCA AGN C GGTGCC A C C A TGA G 1119
QY      808  ACCT TCTGTGG CAC GCG GAG TAT C TCG CAC CTGAG GTG C T TCA ATA G CAG C C T TAT GAC 867
DB      1120  ACCT TTT TCG C CAC ACC C TGA TAC TGTG C C C CCG AGG TGTG GAG GACA AT GACTAC GGC 1179
QY      868  AGN ACTGTG A C TGG TGG TCG C C TGG GAG C TGT C T TGTAT GAG ATG C TGTAT G C C TCG C 927
DB      1180  CGTGC AGT GAG C TGTG GGG G C TGG TGT C ATGTAT G CAG GAT GAT GTG C GGT C G C T G 1239
QY      928  CCT TTTTATAG CCG AAA CAC AGC TGA AATGTAC GACA A C A C T TCTG A A C AAG C C T C T CAG 987
DB      1240  CCT TTT CTA CAC CAG GAC CATG AAG A C T TTTT GAG C TCA T C C T C ATG GAG GAG AT CCG 1299
QY      988  CTG AAA CCA AATATTA CAA ATTCG CCA AGA CAC C C T C TCTG GAG GGC C C T C TCTG CAGA AGG AC 1047

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Db 954 CAAGATCACTGACTTTGGCTCTCGAAGAGGGCATCAGTGACGGGCCACCATGAAAC 1013
Qy 810 CTTCTGTGGCAGCGCGAGTATCTCGCACCTGAGGTGCTTCATAGCAGCCTTATGACAG 869
Db 1014 CTTCTGTGGGACCCGAGTACTTGGCGCTGAGGTGCTGGAGACATGACTATGGCG 1073
Qy 870 GACTGTGGAATGTGGTGGCTCGGAGTGTCTTGTATGAGATGCTGTATGGCTGCGGCC 929
Db 1074 GGCGGTGACTGTGTGGGGCTGGGTGTGCTCATGTACGAGATGATGTGGCGCCCTGCC 1133
Qy 930 TTTTATAGCGGAACACAGCTGAAATGTACGACAACTTGTGAACAGCCTCTCCAGCT 989
Db 1134 CTTCTCAACACAGACACAGAGCCCTCTTGTGAGCTCATCTCATGAAAGAGATCCGCT 1193
Qy 990 GAAACCAATATTAACAAATTCGCAAGACACCTCTGGAGGGCTCTCTCGAAGGACAG 1049
Db 1194 CCGCGCAGCTGAGCCCGGAGCAAGTCCCTGCTTGTGGGTGCTTAAGAGGACCC 1253
Qy 1050 GACAAAGCGGT---CGGGGCAAGGATGACTTCATGAGATTAAGAGTCACTGTCTT 1106
Db 1254 CAAGCAGAGGCTTGGTGGGGCCCGAGCGATGCCAAGAGGTCTATGAGCACAGGTCTT 1313
Qy 1107 CTCCTTAATTAAGTGGATGATCTCATTAATAAGAAATTAAGAAATTAAGAAATTAAG 1166
Db 1314 CTTCAAGATCAACTGGCAGGAGCTGTGTCAGAAAGAGTCTCTGCCACCTTCAAACTCA 1373
Qy 1167 TGTGAGTGGGCCCAACAGCTACGGCAGCTTTGACCCGAGTTTACCGAAGAGCTGTCCC 1226
Db 1374 GGTCACTCGAGGTGACACAGAGTCTTCGATGATGAATTTACCGCCAGTCCATCAC 1433
Qy 1227 CAACTCCATTGGCAAGTCCCTTGACAGCGT 1256
Db 1434 AATCACACCCCTGACCGCTATGACAGCT 1463

RESULT 8

US-09-167-322-3
; Sequence 3, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavoragna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; City: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/167,322
; FILING DATE: 07-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-167-322-3

Query Match 18.6%; Score 248.4; DB 4; Length 1599;
Best Local Similarity 55.7%; Pred. No. 7.9e-70;
Matches 518; Conservative 0; Mismatches 406; Indels 6; Gaps 2;

Qy 330 TGACTTTCACTCTTGAAGTATCGAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAG 389
Db 537 TGACTTCGATATCTCAAACTCCTTGGCAAGGAAACCTTTGGCAAAAGTCTATCTGTGCG 596
Qy 390 ACACAGGAGAGAGAGTGTCTATGACGTCAAAAGTTTACAGAGAAAGCAATCCTGAA 449
Db 597 GGAAAGGCCACTGGCGGCTACTACGCCATGAAGATCTCGAAAGAAAGTCACTCATTCG 656
Qy 450 AAGAAAGAGAGGAGAAACATATATGTGGAGCGGAATGTTCTGTGAAGAAATGTGAAGCA 509
Db 657 CAAGGATGAAGTCGCTCACACAGTCAACGAGAGCCGGGTCTCCAGAACACC---AGGCA 713
Qy 510 CCTTTCTGTGGGGCTTCACTTCTTTCCAGACTGTCTGACAAATTTGACTTTGTCTCT 569
Db 714 CCGCTTCTCACGTGCTGAAGTATGCTTTCCAGACCCACGACCGCTGTGCTTTGTGAT 773
Qy 570 AGACTACATTAATGTGGAGAGTGTCTTACCATCTCCAGAGGAGAGCGTCTTCTGGA 629
Db 774 GGAGTATGCCAACGGGGGTGAGCTGTCTTCCACCTGTCCCGGGAGCGTGTCTTCACAGA 833
Qy 630 ACCACGGGCTCGTTTCTATGCTGCTGAAATAGCAGTGTCTGGGTACCTGCTGATTCAC 689
Db 834 GGAGCGGGCCGGTTTATGGTGCAGAGATTGTCTGGCTCTTGAGTACTTGACCTGCG 893
Qy 690 GAACATCTGTTATAGAGACTTAAACACAGAGAAATATTTGCTAGATTTCACAGGGACACAT 749
Db 894 GGAGCTGGTATACCGGCACATCAAGCTGGAAACCTCATGCTGCACAAAGATGGCCACAT 953
Qy 750 TGTCTTACTGACTTCGGACTCTGCAAGGAGAAACATTGAACACACAGCAACATCCAC 809
Db 954 CAAGATCACTGACTTTTGGCTCTGCAAGAGAGGCGCATCAGTACGGGGCCACCATGAAAC 1013
Qy 810 CTTCTGTGGCAGCGCGAGTATCTCGCACCTGAGGTGCTTCATAAGCAGCCTTATGACAG 869
Db 1014 CTTCTGTGGACCCCGAGTACTCTGGCGCTGAGGTGCTGGAGGACATGACTATGGCG 1073
Qy 870 GACTGTGGAATGTGTGCTGGAGCTGTCTTGTATGAGATGCTGTATGGCTGCGGCC 929
Db 1074 GGCGGTGACTGTGTGGGGCTGGGTGTGCTATGATGAGATGATGTGGCGCCCTGCC 1133
Qy 930 TTTTATAGCGGAACACAGCTGAAATGTACGACAACTTGTGAACAGCCTCTCCAGCT 989
Db 1134 CTTCTCAACACAGGACCCAGCGCTCTTTCGAGCTCATCTCTCATGGAAGAGATCCGCT 1193
Qy 990 GAAACCAATATTAACAAATTCGCAAGACACCTCTCGAGGGCTCTCTGAGAGGACAG 1049
Db 1194 CCGCGCAGCTGACGCCCGAGGCCAAGTCCCTGCTTGTGGCTGCTTGAAGAGGACCC 1253
Qy 1050 GACAAAGCGGT---CGGGGCAAGGATGACTTTCATGGAGATTAAGAGTCACTGTCTTCT 1106
Db 1254 CAAGCAGAGGCTTGGTGGGGCCCGAGCGATGCCAAGAGGTCATGGAGCACAGGTCTT 1313
Qy 1107 CTCCTTAATTAAGTGGATGATCTCATTAATAAGAAATTAAGAAATTAAGAAATTAAG 1166
Db 1314 CTTCAAGATCAACTGGCAGGAGCTGTGTCAGAAAGAGTCTCTGCCACCTTCAAACTCA 1373
Qy 1167 TGTGAGTGGGCCCAACAGCTACGGCAGCTTTGACCCGAGTTTACCGAAGAGCTGTCCC 1226
Db 1374 GGTCACTCGAGGTGACACAGAGTCTTCGATGATGAATTTACCGCCAGTCCATCAC 1433
Qy 1227 CAACTCCATTGGCAAGTCCCTTGACAGCGT 1256

Db 1434 AATCACACCCCTGACCGCTATGACAGCCT 1463

RESULT 9

US-09-225-749-24
 ; Sequence 24, Application US/09225749
 ; Patent No. 6300320
 ; GENERAL INFORMATION:
 ; APPLICANT: Dean, Nicholas M.
 ; APPLICANT: McKay, Robert, A.
 ; TITLE OF INVENTION: Modulation of c-jun using inhibitors of protein kinase C
 ; FILE REFERENCE: ISIS3313
 ; CURRENT APPLICATION NUMBER: US/09/225,749
 ; CURRENT FILING DATE: 1999-01-05
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 24
 ; LENGTH: 2245
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (28)..(2046)
 ; PUBLICATION INFORMATION:
 ; JOURNAL: Nucleic Acids Res.
 ; VOLUME: 18
 ; ISSUE: 8
 ; PAGES: 2183
 ; DATE: 1990-04-25
 ; DATABASE ACCESSION NUMBER: X52479/Genbank
 ; DATABASE ENTRY DATE: 1993-09-12
 ; US-09-225-749-24

Query Match 18.0%; Score 241; DB 4; Length 2245;
 Best Local Similarity 54.9%; Pred. No. 2.5e-67;
 Matches 497; Conservative 0; Mismatches 405; Indels 3; Gaps 1;
 QY 274 AGTCTCTCAGCAATCACTTGGCCGCTGCTCCATCTCATGCTAAACCATCTGAC 333
 DB 982 AGTCCCTCTGAAGCAGGAAACAACTTCCAAACAACTTCAACGAGTGAAACATCGGAC 1041
 QY 334 TTTCACTTCTTGAAGTGATCGGAAAGGCGAGTTTGGAAAGGTTCTCTAGCAAGACAC 393
 DB 1042 TTTCAATTTCTCATGTTGTTGGAAAGGAGTTTGGAAAGGTTGCTTGGCGACAGG 1101
 QY 394 AAGCAGAGAAGTGTTTCTATGCAAGTCAAAAGTTTACAGAAGAAAGCAATCTTGAAGAA 453
 DB 1102 AAGGGCACAGAAGAACTGTATGCAATCAAAATCTGAAGAAGGATGTGGTGAATTCAGGAT 1161
 QY 454 AAGAGGAGAAGCATATATGTGCGAGCGGANTTGTCTTGAAGATGTGAAGCACCCT 513
 DB 1162 GATGACGTGAGTGACCATGTGTGAAGAAAGCGAGTCTTGGCCCTGTGACAAACCCCG 1221
 QY 514 TTTCTGTGGGCTTCACTTCTCTTCCAGACTGCTCAAAATTTGTAATTTGTCCTAGAC 573
 DB 1222 TTTCTGACAGCTGCACTCTGCTTCCAGACAGTGATCGGTGTAATTTGTCATGGA 1281
 QY 574 TACATTAATGTTGAGAGTTGTTCTACCATCTCCAGAGGAAAGCGTCTCTCTGGAACCA 633
 DB 1282 TATGTCAACGGTGGGACCTCATGTACCAATTCAGCAAGTAGGAAATTTAAGGAACCA 1341
 QY 634 CGGCTCGTTCTATGCTGTGAATAGCAGTGCCTTGGCTACCTGCAATTCATGAA 693
 DB 1342 CAAGCAGTATTTCTATGCGGAGAGATTTCATCGGATTTGTTCTTCTATGAAGAGGA 1401
 QY 694 ATCGTTTATAGACTTTAAACACAGAGATATTTTGTAGATTCACAGGAGACATGTC 753
 DB 1402 ATCATTTATAGGGATCTGAAGTTAGATACGTATGTTGATTCAGAGAGACATATCAA 1461
 QY 754 CTTAAGTCTCGGACTCTCAAGGAGAAACATTTGAACACAAACAGCAACATCAACCTTC 813
 DB 1462 ATTGCTGATTTGGGATGTGCAAGGAACACATGATGATGGATGAGTCAAGCAACGAGACCTTC 1521

QY 814 TGTGGCAGCCGAGATATCTCGACCTGAGGTGCTTATAAGCAGCTTATGACAGGACT 873
 DB 1522 TGTGGACTCCAGATTATATATCCCCAGAGATAATCGCTTATCAGCCGTATGGAATCT 1581
 QY 874 GTGAGTGTGTGGCTGCTGGAGCTGTCTTGTATGAGATCTGTATGGCTGCGGCTTTT 933
 DB 1582 GTGGACTGTGGCTTATGGCTGTCTTGTATGAAATGCTTGGCGGAGCGCTCCATTT 1641
 QY 934 TATAGCCGAACACACAGCTGAATGTACGACAACTTCTGAAACAGCTCTCCAGCTGAAA 993
 DB 1642 GATGTGAAGATTGAAGACAGCTATTTTCACTATCATGAGCACAACCTTCTCTATCCA 1701
 QY 994 CAAATATATTACAAATTCGCAAGACACCTCTGGAGGCTCTCTGAGAGGAGACAGACA 1053
 DB 1702 AAATCTTGTCCAGAGGCTGTCTTATCTGCAAGGACTGATGACCAACACACCGAGCC 1761
 QY 1054 AAGCGCT---CGGGCCCAAGGATGATCTTCATGGAGATTAAAGATCATGTCTTCTCTCC 1110
 DB 1762 AAGCGCTGGCTGTGGCTGAGGGGAGAGGAGCGTGAGAGAGCATGCTTCTTCCGG 1821
 QY 1111 TTAATTAAGTGGAGTATCTCATTAATTAAGAGATTACTCCCTTTTAAACCAATGTG 1170
 DB 1822 AGGATCGACTGGGAAACTGGAGAACAGGAGATCCAGCCACCATTTCAAGCCCAAGTG 1881
 QY 1171 AGTGG 1175
 DB 1882 TGTGG 1886

RESULT 10
 5266464-1
 ; Patent No. 5266464
 ; APPLICANT: HOUSEY, GERARD
 ; TITLE OF INVENTION: METHOD OF SCREENING FOR PROTEIN INHIBITORS
 ; AND ACTIVATORS
 ; NUMBER OF SEQUENCES: 3
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/392,073
 ; FILING DATE: 10-AUG-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 154,206
 ; FILING DATE: 10-FEB-1988
 ; SEQ ID NO:1
 ; LENGTH: 2599
 5266464-1

Query Match 17.6%; Score 235.4; DB 6; Length 2599;
 Best Local Similarity 55.2%; Pred. No. 1.7e-65;
 Matches 500; Conservative 0; Mismatches 401; Indels 4; Gaps 2;
 QY 322 AAACATCTGACTTTTCACTTCTTGAAGTATCGGAAAGGCGAGTTTGGAAAGTTCTT 381
 DB 1104 AAACCTGACCGATTTTAACTTCTCTG-TGGTGTGGGAAAGGCGAGTTTGGCAAGTCATG 1162
 QY 382 CTAGCAAGACACAAGGACAGAGAGTGTCTATGCAAGTCAAAAGTTTTACAGAAGAAAGCA 441
 DB 1163 CTCTAGAGCGGAAGGTTACAGATGAATCTATGCGGTGAAGATCTCTGAAGAAAGATGTG 1222
 QY 442 ATCCTGAAAGAAAGAGGAGAGCATATTTATGTCGAGCGGAATGTCTTGTGTGAAGAAT 501
 DB 1223 GTGATCCAAGATGACCATGTGGAGTGCAATGTTGAGAGAGGAGGTGTGCGCCCTGCCT 1282
 QY 502 GTGAAGACCTTTCTGTTGGGCTTCACTTCTCTTTCCAGACTGCTGACAAATTTGTAC 561
 DB 1283 GGAAGCCCTCCATTCCTGACTCAGCTCCATTCCTGCTTCCAGACCATGAGACCGCTCTAC 1342
 QY 562 TTTGCTCTAGACTACATTAATGTTGGAGAGTTGTTCTTACCATCTCCAGAGGGAACGCTGC 621
 DB 1343 TTTGATGAGTATGTGAACGGGGGCGACCTCATGTATCAATCAACAAAGTTGGCGGT 1402
 QY 622 TTTCTGGAACCAAGGCTCGTTTCTATGCTGTGTAATAGCCAGTGCCTTTGGGCTACCTG 681

Db 1403 TTCAAGAGAGCCCATGCTGTATTTTACGCTGCAGAGATTGCCATCGCTCTTTCTTCTTG 1462
Qy 682 CATTCACCTGAACATCGTTTATAGAGACTTAAACACAGAGAAATATTTTGTCTAGATTCACAG 741
Db 1463 CAGAGCAAGGGCATCATTTTACCGTGCCTGAACTTGAACACGCTGATGCTGGATTCCGAG 1522
Qy 742 GGACACATTCCTTACTGACTTCGGACTCTGCAGGAGAACATTTGAACACACAGCACA 801
Db 1523 GGGCACATCAAAATCGCTGCTTTGGCATGTCTAAAGAGAAATATCTGGGATGGGTGACA 1582
Qy 802 ACATCCACCTTCTGTGACCGCGGAGTATCTGCACCTCGAGTGTCTTATAGAGAGCCT 861
Db 1583 ACCAGACATCTGTGCACTCCAGACTCAATTCGCCACAGAGATCAATGCTTATCAGCCC 1642
Qy 862 TATGACAGGACTGTGGACTGGTGTGCTGGGAGCTGTCTTGTATGAGATGCTGTATGGC 921
Db 1643 TAGGAAAGTCTGTGAGCTGGTGGCGTGTGGAGTCTGCTGTATGAAATGTTGGCTGGC 1702
Qy 922 CTGCGGCTTTTATAGCCGAAACACAGCTGAAATGTACGACACATCTTGAACAGCCT 981
Db 1703 CAGGCACCTTTTGAAGGGAGGATGAGGATGAATCTTCCAGTCAATCATGGAGCACAAC 1762
Qy 982 CTCAGCTGAACCAATATTTACAAATTCGCGAAGACACCTCTCGGAGGCGCTCCTGCAG 1041
Db 1763 GTGCGTATCCCAAGTCCATGTCTAAGGAAGCTGTGGCAATCTGCAAGGGCTTAATGACC 1822
Qy 1042 AAGGACAGGACAAAGCGGCTCG---GGGCAAGGATGACTTCATGGAGATTAAGAGTCA 1098
Db 1823 AAACCCAGGACGCGCTGGTGTGGCGCTGAAGGGACGAGACATTAAGGAGCAT 1882
Qy 1099 GTCTTCTTCTTAATTAATCGGATGATCTCATTAATTAAGAGATTAATCTCCCGCTTTT 1158
Db 1883 GCATTTTTCGGTATATCGACTGGGAAACTCGAAGGAGATTCAGCCACCGTAT 1942
Qy 1159 AACCAATCTGATGGGCGCCCAAGCAGCTAGCGACTTTGACCCGAGTTTACCGAAG 1218
Db 1943 AAACCAAAAGCTAGAGACAGGAGACACCTCCAACCTTCACAAAGAGTTTCAACAGCAG 2002
Qy 1219 CTTGT 1223
Db 2003 CTTGT 2007

RESULT 11
US-09-313-930-1
; Sequence 1, Application US/09313930
; Patent No. 6235723
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of Human Protein
; TITLE OF INVENTION: Kinase C-delta Expression
; FILE REFERENCE: ISPH-0357
; CURRENT APPLICATION NUMBER: US/09/313,930
; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2104
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2089)
; PUBLICATION INFORMATION:
; AUTHORS: Aris, J. P.
; AUTHORS: Basta, P. V.
; AUTHORS: Holmes, W. D.
; AUTHORS: Ballas, L. M.
; AUTHORS: Moomaw, C.
; AUTHORS: Rankl, N. B.
; AUTHORS: Blobel, G.
; AUTHORS: Loomis, C. R.
; AUTHORS: Burns, D. J.

; TITLE: Molecular and biochemical characterization of a
; TITLE: recombinant human PKC-delta family member
; JOURNAL: Biochim. Biophys. Acta
; VOLUME: 1174
; ISSUE: 2
; PAGES: 171-181
; DATE: 1993-08-19
; DATABASE ACCESSION NUMBER: L07860
; DATABASE ENTRY DATE: 1993-11-02
US-09-313-930-1

Query Match 17.2%; Score 230.8; DB 4; Length 2104;
Best Local Similarity 54.4%; Pred. No. 4.6e-64;
Matches 491; Conservative 0; Mismatches 402; Indels 9; Gaps 1;

Qy 332 ACTTTCACCTTCTTGAAGTGATCGGAAAGGGAGTTTTCGAAAGGTTTCTTCTAGCAAGAC 391
Db 1101 ACTTTCATCTTCCACAAGTCTCGGCAAGGAGCTTCGGAAAGGTTGCTGCTGGAGAGC 1160
Qy 392 ACAAGCAGAAGAAGTGTCTATGCAAGTCAAAAGTTTTCAGAGAAGAAGCAATCCTGAAAA 451
Db 1161 TGAAGGGCAGAGAGAGATGACTCTGCCATCAAGGCCCTCAAGAGGATGTGGTCTGATCG 1220
Qy 452 AGAAGAGAGAGAGCATATTTATGTCGAGGGGAATGTTCTGTGTAAGAATGTGAAGCACC 511
Db 1221 ACAGACAGCTGGAGTGCACCATGTTTGAAGCGGTGCTGCACACTTGCAGCAGAGAAATC 1280
Qy 512 CTTTCTCTGTGGGCTTCTCTTTCAGACTGCTGACAAATTTGTACTTTTGTCTCTAG 571
Db 1281 CCTTCTCACCACCTCATCTGCACCTTCAGACCAAGGACCACTGTTCTTTTGTATGG 1340
Qy 572 ACTACATTAATGTTGGAGAGTTGTTCTACCATCTCCAGAGGGAACGCTGCTTCTCGAAC 631
Db 1341 AGTTCTCAACGGGGGACCTGATGTACCATCTCAGGACAAAGCGCGCTTTGAACTCT 1400
Qy 632 CAGGGCTCGTTTCTATGCTGTAATAAGCAGTGCCTTGGGCTACCTGCAATCTACTGA 691
Db 1401 ACCGTGCCACGTTTATGCGCTGAGATAATGTGTGAGCTGCGAGTTTCTACAGCAAGG 1460
Qy 692 ACATCGTTTATAGAGACTTAAACACAGAGATAATTTTGTAGATTACAGGGGACACATTG 751
Db 1461 GCATCAATTTACAGGGACCTCAAACTGGACAATGTGCTGTTGGACCGGGATGGCCACATCA 1520
Qy 752 TCCTTACTGATTCGGACTCTGCAAGGAGAAACATTTGAACACAGACACAAACATCCACCT 811
Db 1521 AGATTGCCGACTTTGGGATGTGCAAGAGAAATATTTCCGGGAGAGCGCGGCCAGACCT 1580
Qy 812 TCTGTGGCACCGCGGAGTATCTGCACCTGAGGTGCTTCATAGCAGCCTTATGACAGGA 871
Db 1581 TCTGCGGCACCCCTGACTATATCGCCCTGAGATCTTACAGGGCTTGAAGTACACATCT 1640
Qy 872 CTGTGACCTGTTGCTGCGGAGCTGTTCTGTATGAGATGCTGTATGGCTGCCGCTT 931
Db 1641 CTGTGACCTGTTGCTTTCGGGGTCTTCTGTGTACAGATGCTCATTTGCGGAGTCCCT 1700
Qy 932 TTTATAGCCGAAACACAGCTGAAATGTACGACAAACATTTCTGAACAGGCTCTCCAGCTGA 991
Db 1701 TCCATGCTGATGATGAGGATGAACTCTTCGAGTCCATCCGTGTGGACACGCCACATTATC 1760
Qy 992 AACCAAAATTAACAAATTCGCAAGACACTCTCTGGAGGCTCTCTGCAAGAGGACAGGA 1051
Db 1761 CCGCTGGATCAACAGGAGTCCAAGGACATCTGTGAGAAAGCTCTTTGAAGGAAACCAA 1820
Qy 1052 CAAAGCGCTCGGGCCCAAGGATGACTTTCATGGAGATTGAAGTATGCTTCTTCTCTCT 1111
Db 1821 CCAAGAGGCTGGGAATGACGGGAAAC-----ATCAAAATCCACCCCTCTTCTTCAAGA 1871
Qy 1112 TAATTAACCTGGGATGATCTCAATTAATAAGAGATTACTCCCGCTTTTAAACCCAAATGTGA 1171
Db 1872 CATAAACTGGACTCTGCTGGAAAGCGGAGGTTGAGGCCACCTTCAGGCCCAAAGTGA 1931
Qy 1172 GTGGGCCCAACGACCTTACGGCAGCTTTTGACCCCGAGTTTACCGAAGAGCCTGTCCCCAAT 1231


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; NAME/KEY: CDS
; LOCATION: (95)..(2215)
US-09-429-322-3

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Query Match	16.0%	Score 214.6	DB 4	Length 2754
Best Local Similarity	52.3%	Pred. No. 9.5e-59		
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Qy	281	CTCAGCAAAATCAACCTTTGGCCGTCGTCCTCAATCTCATGCTAAACCATCTGACTTTTCACCT	340	
Db	1179	CTGACTGACACNAAGAAAGACCATCTCTGCAGATTAACTTAAATAATTGAGATTTATCT	1238	
Qy	341	TCTTTGAAAGTGATCGGAAAGGGCAGTTTTTGGAAAGGTTCTTCTTAGCAAGACACAAGGCAG	400	
Db	1239	TGCACAAAATCTTTGGGGAAGGAAGTTTGGCAAGGTCCTCTGGCAGAAATCAAGAAAA	1298	
Qy	401	AAGAAGTGTTCTATGCAGTCAAAAGTTTTTACAGAGAAAGCAATCCTCAAAAAGAAAGAGG	460	
Db	1299	CCAATCAATTTTTTCGCAATTAAGGCCTTTAAAGAAAGATGTGGTCTTGATGGACGATGATG	1358	
Qy	461	AGAAGCATATATGTTCGGAGCGGAATGTCTCTGTGTGAAGAAATGTGAAGCACCCCTTTTCC	520	
Db	1359	TTGAGTGCACGATGGTAGAAGAGAGATCTCTTCTCTTGGCTGGGACCATCCGTTTCTGA	1418	
Qy	521	TGGCCCTTCACTTCTCTTTCAGACTGCTGACAAAATTGTATTTGTCTAGACTACATTA	580	
Db	1419	CGCACATGTTTGTACATTTTTCAGACCAGGAAAAACCTCTTTTGTGTATGGAGTACCTCA	1478	
Qy	581	ATGCTGAGAGTTGTTCTTACCATCTCCAGAGGGAACGCTGCTTCTCGAACCCACGCGCTC	640	
Db	1479	ACGAGGGGACTTAATGTACCAATCAAGCTGCCACAAGTTGCAGCTTTCAGAGCGA	1538	
Qy	641	GTTTCTATGCTGCTGAATAGCCAGTGCCTTGGGCTACCTGCAATTCAGAAATCGTTT	700	
Db	1539	CGTTTATGCTGCTGAAATCATTTCTGGTCTGCAGTTTCTTTCATTCCAAAGGAATAGTCT	1598	
Qy	701	ATAGAGACTTTAAACACAGAGAAATTTTGTGTAGATTACAGAGGACACATTTGCTTACTG	760	
Db	1599	ACAGGACCTTGAAGCTAGATAACATCTCTGTGTAGCAAAGATGGACATATCAAGATCGCG	1658	
Qy	761	ACTTTCGACTCTGCAAGGAGAAATTTGAACACACAGCACAAATCCACCTTCTGTGGCA	820	
Db	1659	ATTTTGAATGTGCAAGGAGAACATGTTAGGAGATGCCAAGACGAATACCTTCTGTGGGA	1718	
Qy	821	CGCCGAGTATCTCGCACTGAGTGCTCTCATAGCAGCCCTTATGACAGACTGTGACT	880	
Db	1719	CACCTGACTACATCGCCCCAGAGATCTTGTGTGGTTCAGAAATACAAACCATCTGTGGA	1778	
Qy	881	GGTGGTCCCTGGGAGCTGCTTGTATCAGATGCTGTATGGCTCGCCGCTTTTATAGCC	940	
Db	1779	GGTGGTCTTCGGGTTCTCTTTATGAAATGCTGATTTGTTCAGTGCCTTTTCCCGGC	1838	
Qy	941	GAACACAGCTGAAATGACGACAAATTTGAAACAAGCCCTCTCCAGCTGAAACCAATA	1000	
Db	1839	AGGATAGGAGGAGCTCTTCCACTCCATCCGATGGACAATCCCTTTTACCACGGTGGC	1898	
Qy	1001	TTACAAATTTCCGGAAGACACTCTCGAGGGCCCTCTGCAAGAGGACAGACAAAGCGGC	1060	
Db	1899	TGGAGAAGGAAGCAAGGACCTCTGTGTGAAGCTCTTTCGTGCGAGAACCTGAGAAGAGGC	1958	
Qy	1061	TCGGGGCCAAAGGATGACTTCATGGAGATTAAAGTCAATGCTTCTTCTCTCTTAATTA	1120	
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Db 2130 A 2130

RESULT 14

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US-09-430-564-1
; Sequence 1, Application US/09430564
; Patent No. 6372467
; GENERAL INFORMATION:
; APPLICANT: John Blenis
; APPLICANT: Kay K. Lee-Fruman
; APPLICANT: Calvin J. Kuo
; TITLE OF INVENTION: P54S6K AND P65S6K GENES, PROTEINS,
; TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
; FILE REFERENCE: 00246/506002
; CURRENT APPLICATION NUMBER: US/09/430,564
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/106,141
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-430-564-1

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Query Match	15.0%	Score 200.2	DB 4	Length 1732
Best Local Similarity	53.9%	Pred. No. 3.1e-54		
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Qy	410	TCATGTCAGTCAAGTTTACAGAAGAAACCAATCTCGAAAGAAAGAGAGGAAGCAT	469	
Db	319	TATATGCCATGAAGTCTTAAGGAAGCCAAAATTTGTGCCAATGCCAAGACACAGCAC	378	
Qy	470	TTATGTGCGAGCGGAATGTTCTGTGAAGAATGTGAAGCACCCCTTTCTCGTGGGCGCTTC	529	
Db	379	ACACAGGGCTGAGCGGAACATTTCTAGAGTCAGTGAAGCACCCCTTTATTGTGGAACGTG	438	
Qy	530	ACTTCTCTTTCCAGACTGTGCAGAAATTTGACTTTGTCTTAGACTACATTAATGGTGGAG	589	
Db	439	CCTATGCTTTCCAGACTGGTGGCAAACTCTACCTCATCTCTTGATGCTCAGTGGTGGCG	498	
Qy	590	AGTTGTTCTACCATCTCCAGAGGAAACGCTGCTTCTGGAACCAACGGGCTGTTTCTATG	649	
Db	499	AGCTCTTACGCACTCGGACGAGAGGGCACTCTTCTGGAAGATACGGCCTGTTCTACC	558	
Qy	650	CTGCTGAATATAGCCAGTGCCCTTGGGCTACCTGCAATCACTGAACATCGTTTATAGAGACT	709	
Db	559	TGGCTGAGATCAAGCTGGGCCCTGGGCCATCTCCACTCCCAAGGCATCATCTACCGGGACC	618	
Qy	710	TAAACACAGAGATATTTTGTCTAGATTACAGGGACACATTTGCTTACTTGACTTCGGAC	769	
Db	619	TCAAGCCGAGAACATCATGCTCAGCAGCCAGGGGCCACATCAAACCTGACCGACTTTGGAC	678	
Qy	770	TCTGCAAGGAGAACATTGAAACAAACAGACAAACATCCACTTCTGTGGCACCGCGAGT	829	
Db	679	TCTGCAAGGAGTCTATCCATGAGGGCGCCTCACTACACCTTCTGCGGCACCAATTGAGT	738	
Qy	830	ATCTCGCACCTGAGTGCTTTATGAAGCAGCCTTTATGACGAGACTGTGGACTGGTGGTCC	889	
Db	739	ACATGGCCCTCGAGATTCTGTCGCGCAGTGGCCACAAACCGGGCTGTGGACTGGTGGAGCC	798	
Qy	890	TGGAGCTGTGTTGATAGATGCTGTATGGCCCTGGCCCTTTTATAGCGGAACACACAG	949	
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Qy	950	CTGAAATGTACGACAAACATTTCTGAACAAGCCTCTCCAGCTGAAACCAAATATTACAAATT	1009	
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Db 919 ATGCCCGGACCTTGTCAAAAGTTTCTGAAACGGAATCCAGCCAGCGAATTGGGGTG 978
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 Qy 1187 TACGGCACTTTGACCCCGAGTTTAC 1211
 Db 1099 TGAGCCAGTTTGATACCGGCTTCAC 1123

RESULT 15

US-08-594-031-164
 ; Sequence 164, Application US/08594031
 ; Patent No. 5783182
 ; GENERAL INFORMATION:
 ; APPLICANT: THOMPSON, Timothy C.
 ; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
 ; NUMBER OF SEQUENCES: 175
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BAKER & BOTTS, L.L.P.
 ; STREET: 1299 Pennsylvania Avenue, N.W.
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20004-2400
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/594,031
 ; FILING DATE: 30-JAN-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/006,838
 ; FILING DATE: 16-NOV-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Remenick, James
 ; REGISTRATION NUMBER: 36,902
 ; REFERENCE/DOCKET NUMBER: 0A146-0110
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-639-7700
 ; TELEFAX: 202-639-7890
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 164:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 266 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; US-08-594-031-164

Query Match 13.9%; Score 185.6; DB 1; Length 266;
 Best Local Similarity 91.2%; Pred. No. 4.5e-50;
 Matches 219; Conservative 0; Mismatches 19; Indels 2; Gaps 2;
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 Qy 380 TTCTAGCAACACAAAGCGAGAGAGTGTCTATGCAGTCAAAGTTTACAGAGAAAG 439

Db 88 TTCTGGCTAGGCACAAAGGCAGAGAAAGTATTCTATGCAGTCAAAGTTTACAGAAG-AAG 146
 Qy 440 CAATCCTGAAAGAAAGAGAGGAGAGCATATTATGTCCGAGCGGAATGTTCTGTGAAGA 499
 Db 147 CCATCCTGAAAGAAAGAGAGGAGCATATTATGTCAAGAGCGGAATGTTCTGTGAAGA 206
 Qy 500 ATGTGAAGCACCCCTTTTCTGTGGGCTTTCACCTTCTTTTCCAGACTGCTGACAAATTTGT 559
 Db 207 ATGTGAAGCACCCCTTTTCTGTGGGCTTTCACCTTCTTTTCCAGACTGCTGACAGCTCT 266

Search completed: June 25, 2003, 09:41:50
 Job time : 66 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 05:48:04 ; Search time 239 Seconds
(without alignments)
12607.422 Million cell updates/sec

Title: US-10-067-977-1

Perfect score: 1338

Sequence: 1 atggggagagcagggcgc.....ccacggactcttctctga 1338

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125995159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*

24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1219.8	91.2	2311	19	AAV23833 Human protein kina
2	1218.2	91.0	1296	22	AAF44639 Novel protein kina
3	1218.2	91.0	2346	20	AAV74190 Human sgk DNA, Ho
4	1218.2	91.0	2370	19	AAV48311 Human cell-volume
5	1218.2	91.0	2370	24	ABK84749 Human cDNA differe
6	1218.2	91.0	2370	24	ABN97360 Gene #3858 used to
7	1218.2	91.0	2370	24	ABL70006 Pancreas cancer re
8	1144	85.5	2281	20	AAZ33647 Human breast tumou
9	983	73.5	2365	21	AAA46592 DNA encoding a rat

10	978.8	73.2	2432	22	AAF44640 Novel protein kina
11	527.2	39.4	1366	22	AAS44987 Novel protein kina
12	527.2	39.4	1812	22	AAF44737 Human serum and g1
13	527.2	39.4	1812	24	AAD36141 Human serum and g1
14	527.2	39.4	1834	21	AAZ27856 Human serum and g1
15	527.2	39.4	2146	21	AAZ27857 Human serum and g1
16	520.4	38.9	2404	21	AAZ27858 Human serum and g1
17	520.4	38.9	2512	20	AAV99653 Human serum glucoc
18	520.4	38.9	2572	23	ABK43712 DNA encoding novel
19	520.4	38.9	2702	23	ABK43558 Human polynucleoti
20	520.4	38.9	2711	22	AAI59776 Human polynucleoti
21	517.2	38.7	2760	22	AAI57990 Human protein enco
22	516.2	38.6	1333	22	AAH99535 Human serine thro
23	515.6	38.5	3019	21	AAH99248 Human prostate can
24	410.4	30.7	423	21	AAF16425 Novel protein kina
25	356.2	26.6	1346	22	AAF44641 Novel protein kina
26	351.6	26.3	851	22	AAS27021 DNA encoding nove
27	351.6	26.3	851	23	ABK43988 DNA encoding novel
28	348.8	26.1	2483	22	AAK94684 Human full-length
29	306.4	22.9	449	21	AAC03936 Human secreted pro
30	283.8	21.2	2375	23	ABL19107 Drosophila melanog
31	283.8	21.2	2425	23	ABL28911 Human colon specif
32	283.8	21.2	3872	24	ABA91312 Novel protein kina
33	282.4	21.1	2250	22	AAF44642 Wild type murine A
34	259.4	19.4	2626	21	AAO9078 Mouse Akt cDNA. M
35	259.4	19.4	2626	24	AAZ28550 Human Akt-3 coding
36	258.8	19.3	1440	21	AAAG2451 Human Akt3 encodin
37	258.8	19.3	1440	24	ABL50839 Human Akt-3 nucleo
38	258.8	19.3	1547	21	AAAG2450 DNA encoding a hum
39	258.8	19.3	1570	21	AAA96637 Human Akt3 encodin
40	258.8	19.3	1570	22	AAH79025 Human serine/threo
41	258.8	19.3	1570	22	AAH89264 DNA encoding a hum
42	258.8	19.3	2367	21	AAAC61592 Human low adenosin
43	258.6	19.3	2574	21	AAF21406 Human adenosine re
44	258.6	19.3	2574	21	AAA35284 Human cDNA differe
45	258.6	19.3	2574	24	ABK84515

ALIGNMENTS

RESULT 1

AAV23833

ID AAV23833 standard; cDNA; 2311 BP.

XX

AC AAV23833;

XX

DT 31-JUL-1998 (first entry)

XX

DE Human protein kinase HPK-3 coding sequence.

XX

KW Protein kinase; human; HPK; signalling cascade; kinase expression;

KW Alzheimer's disease; cancer; anti-inflammatory agent; immunosuppressor;

KW asthma; multiple sclerosis; rheumatoid arthritis; lymphocytic leukaemia;

KW lymphoma; therapy; ss.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS 379..1080

FT

FT /*tag= a

XX

PN WO9811234-A2.

XX

PD 19-MAR-1998.

XX

PF 10-SEP-1997; 97WO-US15923.

XX

PR 12-SEP-1996; 96US-0712709.

XX

PA (INCY-) INCYTE PHARM INC.

XX

PI Au-Young J, Guegler KJ, Hawkins PR;

XX WPI: 1998-207394/18.
 DR P-PSDB; AAM54205.
 XX
 PT New isolated human protein kinase(s) - used to develop products for
 PT diagnosis and treatment of e.g. Alzheimer's disease, cancers,
 PT asthma, multiple sclerosis or rheumatoid arthritis
 XX
 PS Claim 25; Fig 3; 75pp; English.
 XX
 CC This sequence encodes a human protein kinase (HPK) of the invention. The
 CC HPK protein can be used to develop products for studying signalling
 CC cascades in various cells and tissues, diagnosing disease and selecting
 CC inhibitors or drugs with the potential to intervene in various disorders
 CC or diseases in which altered kinase expression is implicated. The
 CC products can be used to e.g. reverse memory loss such as due to
 CC Alzheimer's disease, for cancer treatment or to provide anti-inflammatory
 CC and immunosuppressive effects in the treatment of e.g. asthma, multiple
 CC sclerosis, rheumatoid arthritis, as well as certain cancers, e.g.
 CC lymphocytic leukaemias or lymphomas.
 XX
 SQ Sequence 2311 BP; 604 A; 508 C; 506 G; 692 T; 1 other;
 Query Match 91.2%; Score 1219.8; DB 19; Length 2311;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 116 TGGCTTTCATGAAGCAGAGAGAGATGGTCTGAACGACTTTATTCAGAGATTGCCAATA 175
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 DB 143 ACTCCATGATGATGCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 202
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 DB 203 AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTCTCAGCAAAATCAACC 262
 QY 296 TTGGCCCGTCTGCAATCTCTATGCTGAACCATCTGACTTTCACTTTGAAAGTATCG 355
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 DB 683 CAGAGATATTTGCTAGATTTCAGGAGACACATTTGCTTACTGACTTCGGACTCTGCA 742
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DB 743 AGGAGAACTTGAACACACACAGCACAACATCCACCTTCTGTGGCAGCCGCGAGTATCTCG 802
 QY 836 CACCTGAGTGTCTTATAGCAGAGCTTATGACAGGACTGTGACTGGTGGTGGGAG 895
 DB 803 CACCTGAGTGTCTTATAGCAGAGCTTATGACAGGACTGTGACTGGTGGTGGGAG 862
 QY 896 CTGTCTTGTATGAGATGCTGTATGCTTCCGCTTCTTATAGCCGAAACACAGCTGAAA 955
 DB 863 CTGTCTTGTATGAGATGCTGTATGCTTCCGCTTCTTATAGCCGAAACACAGCTGAAA 922
 QY 956 TGTACGACAACTTGTAAACAGCTTCCAGCTGAAACCAATATTAATAATTCGCGAA 1015
 DB 923 TGTACGACAACTTGTAAACAGCTTCCAGCTGAAACCAATATTAATAATTCGCGAA 982
 QY 1016 GACACTCTCTGAGGCTCTCTGCAAGGAGCAGGACGAGGCTCGGGGCGCAGGATG 1075
 DB 983 GACACTCTCTGAGGCTCTCTGCAAGGAGCAGGACGAGGCTCGGGGCGCAGGATG 1042
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 QY 1316 CTCCACGAGCTTTTCTCTCA 1338
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 RESULT 2
 AAF44639
 ID AAF44639 standard; cdNA; 1296 BP.
 XX
 AC AAF44639;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Novel protein kinase cdNA, SEQ ID NO: 18.
 XX
 KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;
 KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
 OS Homo sapiens.
 XX
 PN WO200073469-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US14042.
 XX
 PR 28-MAY-1999; 99US-0136503.
 XX
 PA (SUGS-) SUGEN INC.
 XX
 PI Flowman GD, Martinez R, Whyte D, Sudersanam S;
 XX
 DR WPI; 2001-032161/04.
 DR P-PSDB; AAB65613.
 XX

PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 XX neurodegenerative diseases and/or cancers -
 PS Disclosure; Fig 2; 310pp; English.
 XX
 CC The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomyopathies, strokes, renal failure,
 CC oxidative-stress related disorders, chronic inflammatory bowel disease,
 CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
 CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
 CC reproductive disorders.
 XX
 SQ Sequence 1296 BP; 345 A; 333 C; 293 G; 325 T; 0 other;

Query Match 91.0%; Score 1218.2; DB 22; Length 1296;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 116 TGCGTTTCATGAAGCAGAGAGAGATGGTCTGAACGACTTTATTCAGAGATTGCCAATA 175
 DB 74 TCCTTTTCATGAAGCAGAGAGAGATGGTCTGAACGACTTTATTCAGAGATTGCCAATA 133

QY 176 ACTCCTATGATCATCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235
 DB 134 ACTCCTATGATCATCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 193

QY 236 AGCCTGAGCTTATGAATGCCAACCCCTTCTCCTCCACCAAGTCTCTCAGCAATCAACC 295
 DB 194 AGCCTGAGCTTATGAATGCCAACCCCTTCTCCTCCACCAAGTCTCTCAGCAATCAACC 253

QY 296 TTGGCCCGTCTGCTCAATCTCATGCTAAACCTCTGACTTTTCACTTTTCACTTTTCACTTTCT 355
 DB 254 TTGGCCCGTCTGCTCAATCTCATGCTAAACCTCTGACTTTTCACTTTTCACTTTTCACTTTCT 313

QY 356 GAAAGGCGAGTTTGGAAAGTTTCTCTACGACAGACACAGGCGAGAGAGTCTTCTATG 415
 DB 314 GAAAGGCGAGTTTGGAAAGTTTCTCTACGACAGACACAGGCGAGAGAGTCTTCTATG 373

QY 416 CAGTCAAAAGTTTTCAGAGAAAGCAATCTGAAAGAAAGAGAGAGCAATATTATGT 475
 DB 374 CAGTCAAAAGTTTTCAGAGAAAGCAATCTGAAAGAAAGAGAGAGCAATATTATGT 433

QY 476 CGAGCGGAATGTTCTGTTGAAGAAATGTGAAGCACCCCTTTCCTGGGGCTTCACTTCT 535
 DB 434 CGAGCGGAATGTTCTGTTGAAGAAATGTGAAGCACCCCTTTCCTGGGGCTTCACTTCT 493

QY 536 CTTTCCAGAGCTGCTGACAAATTTGCTTCTCTAGACTACATTAATGTTGGAGAGTTGT 595
 DB 494 CTTTCCAGAGCTGCTGACAAATTTGCTTCTCTAGACTACATTAATGTTGGAGAGTTGT 553

QY 596 TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCAAGGCTGCTTCTATGCTGCTG 655
 DB 554 TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCAAGGCTGCTTCTATGCTGCTG 613

QY 656 AAATAGCCAGTCTTGGGCTACCTGCATTTCATCTGAACATCGTTTATAGAGACTTAAAC 715
 DB 614 AAATAGCCAGTCTTGGGCTACCTGCATTTCATCTGAACATCGTTTATAGAGACTTAAAC 673

QY 716 CAGAGAAATATTTGCTAGATTTCAGGGACACATTGCTTACTGACTTCGGACTCTGCA 775
 DB 674 CAGAGAAATATTTGCTAGATTTCAGGGACACATTGCTTACTGACTTCGGACTCTGCA 733

776 AGGAGAACATTGAACACAAACAGACAAATCCACACTTCTGTGGCAGCCGGAGTATCTCG 835
 734 AGGAGAACATTGAACACAAACAGACAAATCCACACTTCTGTGGCAGCCGGAGTATCTCG 793

836 CACCTGAGTGTCTCATAGCAGCCTTATGACAGGACTGTGGACTGGTGGTCTGGGAG 895
 794 CACCTGAGTGTCTCATAGCAGCCTTATGACAGGACTGTGGACTGGTGGTCTGGGAG 853

896 CTGCTTGTATGAGATGCTGTATGGCTCGCGCTTTTATAGCCGAAACACACAGCTGAAA 955
 854 CTGCTTGTATGAGATGCTGTATGGCTCGCGCTTTTATAGCCGAAACACACAGCTGAAA 913

956 TGTACGACAACTTCTGAACAGCCTCTCAGCTGAAACCAATATTACAAATTCGCGAA 1015
 914 TGTACGACAACTTCTGAACAGCCTCTCAGCTGAAACCAATATTACAAATTCGCGAA 973

1016 GACACTCTCTGGAGGCTCTTCGACAGAGACAGCAAGCGGCTCGGGGCCAAGATG 1075
 974 GACACTCTCTGGAGGCTCTTCGACAGAGACAGCAAGCGGCTCGGGGCCAAGATG 1033

1076 ACTTCATGAGATTAAAGAGTCATGCTTCTTCTCCTTAATTAACCTGGGATGATCTCATTA 1135
 1034 ACTTCATGAGATTAAAGAGTCATGCTTCTTCTCCTTAATTAACCTGGGATGATCTCATTA 1093

1136 ATAAGAAGATTACTCCCTCTTTAACCCAAATGTGAGTGGGCCCAACGACCTACGGCACT 1195
 1094 ATAAGAAGATTACTCCCTCTTTAACCCAAATGTGAGTGGGCCCAACGACCTACGGCACT 1153

1196 TTGACCCCGAGTTTACGAGAGCCTGTCCCACTCCATTTGGCAAGTCCCTTCATGACAGCG 1255
 1154 TTGACCCCGAGTTTACGAGAGCCTGTCCCACTCCATTTGGCAAGTCCCTTCATGACAGCG 1213

1256 TCTCTGTACAGCCAGCGTCAAGGAGCTGCGAGGCTTTCTAGGCTTTTCTATGCGCG 1315
 1214 TCTCTGTACAGCCAGCGTCAAGGAGCTGCGAGGCTTTCTAGGCTTTTCTATGCGCG 1273

1316 CTCCACGGACTCTTTCTCTCTGA 1338
 1274 CTCCACGGACTCTTTCTCTCTGA 1296

RESULT 3
 AAV74190
 ID AAV74190 standard; DNA; 2346 BP.
 XX
 AC AAV74190;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Human sgk DNA.
 XX
 KW Serum glucocorticoid regulated kinase; sgk; human; treatment; inhibitor;
 KW serine/chronic protein kinase family; antagonist; diabetic nephropathy;
 KW chronic renal failure; inflammation; Alzheimers disease; wound; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 45..1340
 FT /*tag= a
 FT /product= "sgk"
 FT /transl_except= (pos:1185..1187, aa:Asp)
 XX
 PN EP887081-A2.
 XX
 PD 30-DEC-1998.
 XX
 PF 27-MAY-1998; 98EP-0304189.
 XX
 PR 27-JUN-1997; 97US-0051124.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.

PT New nucleic acid encoding cell-volume regulating kinase h-egk and
 PT related proteins - used for diagnosis and treatment of diseases
 PT involving changes in cell volume, e.g. renal insufficiency,
 PT inflammation, infections etc.
 XX
 PS Disclosure; Fig 1; 15pp; German.
 XX

CC The human cell-volume regulating kinase h-egk is inhibited by the
 CC swelling of cells (or presence of urea), whereas cell shrinkage
 CC stimulates its expression. The nucleic acid h-egk, and fragments, are
 CC particularly used to detect changes in cell volume, specifically for
 CC diagnosis of conditions that involve such changes, e.g. hyper- and hypo-
 CC natriemia, diabetes mellitus, renal insufficiency, hypercatabolism,
 CC hepatic encephalopathy, inflammation, microbial/viral infection, fructose
 CC intolerance, hyper- and hypo-glycaemia and Alzheimer's disease.
 CC The nucleic acid, protein and products including receptors that bind
 CC h-egk, can be used to treat these disorders.
 XX

SQ Sequence 2370 BP; 636 A; 517 C; 513 G; 704 T; 0 other;
 Query Match 91.0%; Score 1218.2; DB 19; Length 2370;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	116	TGGCTTTCATGAAGCAGAGGAGGATGGTCTGAACGACTTTATTCAGAGATTGCCAATA	175
Db	116	TCGCTTTTCATGAAGCAGAGGAGGATGGTCTGAACGACTTTATTCAGAGATTGCCAATA	175
Qy	176	ACTCCTATGATGCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG	235
Db	176	ACTCCTATGATGCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG	235
Qy	236	AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCCAAGTCTCTTCAGCAAAATCAACC	295
Db	236	AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCCAAGTCTCTTCAGCAAAATCAACC	295
Qy	296	TTGGCCCGTCGTCCTCATGCTAAACATCTGACTTTCACCTTTCTTGAAGTGTATG	355
Db	296	TTGGCCCGTCGTCCTCATGCTAAACATCTGACTTTCACCTTTCTTGAAGTGTATG	355
Qy	356	GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAGACACACGAGGAGAGAGTGTCTATG	415
Db	356	GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAGACACACGAGGAGAGAGTGTCTATG	415
Qy	416	CAGTCAAAAGTTTACAGAAAGCAATCTGAAAGAAAGAGAGAGCAATATATGT	475
Db	416	CAGTCAAAAGTTTACAGAAAGCAATCTGAAAGAAAGAGAGAGCAATATATGT	475
Qy	476	CGGAGCGGAATGTTCTTGAAGAAATGTGAAGACCCCTTCTCTGGTGGGCTTCACTTCT	535
Db	476	CGGAGCGGAATGTTCTTGAAGAAATGTGAAGACCCCTTCTCTGGTGGGCTTCACTTCT	535
Qy	536	CTTTCAGAGTGTGCAAAATGTTACTTGTCTAGACTACATTAATGTTGGAGAGTTGT	595
Db	536	CTTTCAGAGTGTGCAAAATGTTACTTGTCTAGACTACATTAATGTTGGAGAGTTGT	595
Qy	596	TCTACCATCTCCAGAGGAAAGCTGCTTCTGGAACCAACGAGTCTGTTCTATGCTGCTG	655
Db	596	TCTACCATCTCCAGAGGAAAGCTGCTTCTGGAACCAACGAGTCTGTTCTATGCTGCTG	655
Qy	656	AAATAGCCAGTGTCTGGGCTACCTGCAATTCAGTGAACATCGTTTATAGAGACTTAAAC	715
Db	656	AAATAGCCAGTGTCTGGGCTACCTGCAATTCAGTGAACATCGTTTATAGAGACTTAAAC	715
Qy	716	CAGAGAAATTTGCTAGATTCAGAGGACACATTTCTTACTGATTTTCGGACTCTGCA	775
Db	716	CAGAGAAATTTGCTAGATTCAGAGGACACATTTCTTACTGATTTTCGGACTCTGCA	775
Qy	776	AGGAGAAATTTGCTAGATTCAGAGGACACATTTCTTACTGATTTTCGGACTCTGCA	835
Db	776	AGGAGAAATTTGCTAGATTCAGAGGACACATTTCTTACTGATTTTCGGACTCTGCA	835
Qy	836	CACCTGAGGTGCTTTCATGAAGCAGCCTTATGACAGGACTGTGGACTGTGCTGGGAG	895

Db	836	CACCTGAGGTGCTTTCATGAAGCAGCCTTATGACAGGACTGTGGACTGTGCTGGGAG	895
Qy	896	CTGTCTTGTATGAGATGCTGTATGGCTGCTGCTTTTATAGCCGAAACACAGCTGAAA	955
Db	896	CTGTCTTGTATGAGATGCTGTATGGCTGCTGCTTTTATAGCCGAAACACAGCTGAAA	955
Qy	956	TGTACGACAACTTCTGAACAAAGCCTCTCAGCTGAACCAAAATATTTACAAATTCGCAA	1015
Db	956	TGTACGACAACTTCTGAACAAAGCCTCTCAGCTGAACCAAAATATTTACAAATTCGCAA	1015
Qy	1016	GACACTCTCTGGAGGCTCTCTCAGAGGACAGGACAAAGCGGCTCGGGGCCAAGGATG	1075
Db	1016	GACACTCTCTCTGGAGGCTCTCTCAGAGGACAGGACAAAGCGGCTCGGGGCCAAGGATG	1075
Qy	1076	ACTTATGAGATTAAGAGTCAATGCTTCTTCTCTTAAATTAATGAGTGTCTCATTA	1135
Db	1076	ACTTATGAGATTAAGAGTCAATGCTTCTTCTCTTAAATTAATGAGTGTCTCATTA	1135
Qy	1136	ATAAGAGATTAATCTCCCTCTTAAACCAAAATGAGTGGGCCCAACGACTACGGCACT	1195
Db	1136	ATAAGAGATTAATCTCCCTCTTAAACCAAAATGAGTGGGCCCAACGACTACGGCACT	1195
Qy	1196	TTGACCCGAGTTTACGAAAGAGCCTGTCCCAACTCCATTGGCAAGTCCCTTGACAGCG	1255
Db	1196	TTGACCCGAGTTTACGAAAGAGCCTGTCCCAACTCCATTGGCAAGTCCCTTGACAGCG	1255
Qy	1256	TCCTGCTCAGCCAGGCTCAAGGAAGCTGCGAGGCTTTCCTAGGCTTTCTTATGCGC	1315
Db	1256	TCCTGCTCAGCCAGGCTCAAGGAAGCTGCGAGGCTTTCCTAGGCTTTCTTATGCGC	1315
Qy	1316	CTCCACGAGCTCTTCTCTCTGA 1338	
Db	1316	CTCCACGAGCTCTTCTCTCTGA 1338	

RESULT 5

ABK84749	ABK84749	standard; cDNA; 2370 BP.
ID	ABK84749	
AC	ABK84749;	
XX		
DT	14-AUG-2002 (first entry)	
XX		
DE	Human cDNA differentially expressed in granulocytic cells #1320.	
XX		
KW	Human; ss; granulocytic cell; DNA chip; bacterial infection;	
KW	viral infection; parasitic infection; protozoal infection;	
KW	fungal infection; sterile inflammatory disease; psoriasis;	
KW	rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;	
KW	cardiac reperfusion injury; renal reperfusion injury; ARDS;	
KW	adult respiratory distress syndrome; inflammatory bowel disease;	
KW	Crohn's disease; ulcerative colitis; periodontal disease;	
KW	granulocyte activation; chronic inflammation; allergy.	
OS	Homo sapiens.	
XX		
PN	WO200228999-A2.	
XX		
PD	11-APR-2002.	
XX		
PF	03-OCT-2001; 2001WO-US30821.	
XX		
PR	03-OCT-2000; 2000US-237189P.	
XX		
PA	(GENE-) GENE LOGIC INC.	
XX		
PI	Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;	
XX		
DR	WPI; 2002-435328/46.	
XX		
PT	Detecting granulocyte activation by detecting differential expression	
PT	of genes associated with granulocyte activation, which serves as	

diagnostic markers that is useful for monitoring disease states and drug toxicity

Claim 1; SEQ ID No 1320; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA.

Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query March 91.08; Score 1218.2; DB 24; Length 2370; Best Local Similarity 99.8%; Pred. No. 0; Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

116 TGGCTTTTCATGAAGCAGAGGAGGATGGTCTGAACGACTTTATTTCAGAAAGATTGCCAATA 175
|||||
116 TCGCTTTTCATGAAGCAGAGGAGGATGGTCTGAACGACTTTATTTCAGAAAGATTGCCAATA 175

176 ACTCTATGATGCAACACCTGAAGTTGAGTCCATCTTTGAAAGATCTCCAAACCTCAGG 235
|||||
176 ACTCTATGATGCAACACCTGAAGTTGAGTCCATCTTTGAAAGATCTCCAAACCTCAGG 235

236 AGCTGAGCTTATGAATGCAACCTCTCTCTCCACCAAGTCTCTCAGCAATCAACC 295
|||||
236 AGCTGAGCTTATGAATGCAACCTCTCTCTCCACCAAGTCTCTCAGCAATCAACC 295

296 TTGGCCCGTCTGCTCAATCTCATGCTAAACCATCTGACTTTTCACTTTCTTGAAGATGATCG 355
|||||
296 TTGGCCCGTCTGCTCAATCTCATGCTAAACCATCTGACTTTTCACTTTCTTGAAGATGATCG 355

356 GAAAGGCGAGTTTGGAAAGGTTCTTTAGCAAGACACAAGGCGAGAGAGTGTCTTATG 415
|||||
356 GAAAGGCGAGTTTGGAAAGGTTCTTTAGCAAGACACAAGGCGAGAGAGTGTCTTATG 415

416 CAGTCAAAAGTTTACAGAAAGAGCATCTGTAAGAGAGAGAGGAGAGCATATTATGT 475
|||||
416 CAGTCAAAAGTTTACAGAAAGAGCATCTGTAAGAGAGAGAGGAGAGCATATTATGT 475

476 CGGAGCGGAATGTTCTGTTGAAGAAATGTGAAGCACCCTTTCTCTGGTGGGCTTCACTTCT 535
|||||

Db CGGAGCGGAATGTTCTGTTGAAGAAATGTGAAGCACCCTTTCTCTGGTGGGCTTCACTTCT 535
QY CTTTCCAGACTGCTGACAAATTTGTACTTTGTCTAGACTACATTAAATGTTGGAGATTGT 595
Db CTTTCCAGACTGCTGACAAATTTGTACTTTGTCTAGACTACATTAAATGTTGGAGATTGT 595
QY TCTACCATCTCCAGAGGGAACGCTGCTTCTCGAACCACGGGCTCGTTTCTATGCTGCTG 655
Db TCTACCATCTCCAGAGGGAACGCTGCTTCTCGAACCACGGGCTCGTTTCTATGCTGCTG 655
QY AAATAGCCAGTGCCTTGGGCTACCTGCAATTCACCTGAACATCGTTTATAGAGACTTAAAC 715
Db AAATAGCCAGTGCCTTGGGCTACCTGCAATTCACCTGAACATCGTTTATAGAGACTTAAAC 715
QY CAGAGAAATTTTGTCTAGATTACAGGGACACATTTGCTTACTGACTTCGGACTCTGCA 775
Db CAGAGAAATTTTGTCTAGATTACAGGGACACATTTGCTTACTGACTTCGGACTCTGCA 775
QY AGGAGAAATTTGAACAACACAGCAACATCCACCTTCTGTGCGACGCCGGAGTATCTCG 835
Db AGGAGAAATTTGAACAACACAGCAACATCCACCTTCTGTGCGACGCCGGAGTATCTCG 835
QY CACCTGAGTGTCTTCAATAGCAGCCTTATGACAGGACTGTGACTGGTGTCTGGGAG 895
Db CACCTGAGTGTCTTCAATAGCAGCCTTATGACAGGACTGTGACTGGTGTCTGGGAG 895
QY CTGCTTTGTATGAGATGCTGTATGGCTCGCGCTTTTATAGCCGAAACACAGCTGAAA 955
Db CTGCTTTGTATGAGATGCTGTATGGCTCGCGCTTTTATAGCCGAAACACAGCTGAAA 955
QY TGTACGACAACTTCTGAACAAGCCTCTCCAGCTGAACCAAAATATTACAAATTCGCA 1015
Db TGTACGACAACTTCTGAACAAGCCTCTCCAGCTGAACCAAAATATTACAAATTCGCA 1015
QY GACACCTCTCGAGGCTCTCTCGAAGCAGGACAAAGCGGCTCGGGGCGCAAGGATG 1075
Db GACACCTCTCGAGGCTCTCTCGAAGCAGGACAAAGCGGCTCGGGGCGCAAGGATG 1075
QY ACTTCATGAGATTAAGAGTCAATGCTTCTCTCTTAATTAATCGGATGATCTCATTA 1135
Db ACTTCATGAGATTAAGAGTCAATGCTTCTCTCTTAATTAATCGGATGATCTCATTA 1135
QY ATAAAGAAATTAATCTCCCTCTTTTAAACCAATGTAGTGGGCCCAACGACTACGCACT 1195
Db ATAAAGAAATTAATCTCCCTCTTTTAAACCAATGTAGTGGGCCCAACGACTACGCACT 1195
QY TTGACCCCGAGTTTACCGAAGAGCCTGTCCCAACTCCATTGGCAAGTCCCTTGACAGCG 1255
Db TTGACCCCGAGTTTACCGAAGAGCCTGTCCCAACTCCATTGGCAAGTCCCTTGACAGCG 1255
QY TCTCTGTACAGCAGCGCTCAAGGAAGCTGCGAGGCTTTCTTAGGCTTTTCTATGCGC 1315
Db TCTCTGTACAGCAGCGCTCAAGGAAGCTGCGAGGCTTTTCTTAGGCTTTTCTATGCGC 1315
QY CTCACAGGACTCTTTCTCTCTGA 1338
Db CTCACAGGACTCTTTCTCTCTGA 1338

RESULT 6

ABN97360
ID ABN97360 standard; DNA; 2370 BP.
XX
AC ABN97360;
XX
DT 13-AUG-2002 (first entry)
XX
DE Gene #3858 used to diagnose liver cancer.
XX
KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.

XX OS Homo sapiens.
 XX PN WO200229103-A2.
 XX PD 11-APR-2002.
 XX PF 02-OCT-2001; 2001WO-US30589.
 XX PR 02-OCT-2000; 2000US-237054P.
 XX PA (GENE-) GENE LOGIC INC.
 XX PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
 XX DR WPI; 2002-426119/45.
 XX PT Diagnosing and detecting the progression of liver cancer,
 PT hepatocellular carcinoma or metastatic liver tumor in a patient,
 PT involves detecting the level of expression of two or more genes in a
 PT liver tissue sample
 XX PS Claim 1; SEQ ID NO 3858; 298pp; English.
 XX CC The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
 CC tumour in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient, involving detecting the level of
 CC expression of two or more genes represented in ABN97455 in a
 CC tissue sample. The method of the invention has hepatocytic, and
 CC cytosolic activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,
 CC drug toxicity, drug efficacy and drug metabolism.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 2370 BP; 636 A; 517 C; 513 G; 704 T; 0 other;

Query Match 91.0%; Score 1218.2; DB 24; Length 2370;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 116 TGGCTTTCATGACGACGAGGAGTGGTCTGACGACTTTATTCAGAGATTGCCAATA 175
 DB 116 TCGCTTTTCATGAAAGCAGAGGAGATGGGTCTGAACGACTTTATTCAGAGATTGCCAATA 175
 QY 176 ACTCCTATGATGCAACACCCCTGAAGTTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235
 DB 176 ACTCCTATGATGCAACACCCCTGAAGTTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235
 QY 236 AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTCTCAGCAAAATCAACC 295
 DB 236 AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTCTCAGCAAAATCAACC 295
 QY 296 TTGGCCCGTCTCCATCTCATGCTTAACCATCTGACTTTTCACTTTTGAAGTATGTCG 355
 DB 296 TTGGCCCGTCTCCATCTCATGCTTAACCATCTGACTTTTCACTTTTGAAGTATGTCG 355
 QY 356 GAAAGGCGAGTTTGGAAAGTTCTTCTAGCAAGACACAAGGCGAAGAGTGTCTATG 415
 DB 356 GAAAGGCGAGTTTGGAAAGTTCTTCTAGCAAGACACAAGGCGAAGAGTGTCTATG 415
 QY 416 CAGTCAAAGTTTACAGAAAGCAATCTCTGAAAGAAAGAGGAGCAATATATGT 475
 DB 416 CAGTCAAAGTTTACAGAAAGCAATCTCTGAAAGAAAGAGGAGCAATATATGT 475
 QY 476 CGAGCGGAATGTCTGTGAAGAAATGTGAAGACCCCTTCTCGTGGGGCTTCACTTCT 535
 DB 476 CGAGCGGAATGTCTGTGAAGAAATGTGAAGACCCCTTCTCGTGGGGCTTCACTTCT 535

QY 536 CTTTCCAGACTGCTGACAAATTTGTACTTTGTCTAGACTACATTAATGTGGAGAGTTGT 595
 DB 536 CTTTCCAGACTGCTGACAAATTTGTACTTTGTCTAGACTACATTAATGTGGAGAGTTGT 595
 QY 596 TCTACCATCTCCAGAGGGAACGCTGCTTCTGGACACGCGGCTCGTTTCTATGCTGCTG 655
 DB 596 TCTACCATCTCCAGAGGGAACGCTGCTTCTGGACACGCGGCTCGTTTCTATGCTGCTG 655
 QY 656 AAATAGCCAGTGCCTTTGGGCTACCTGCATTCACTGAACATCGTTTATAGAGACTTAAAC 715
 DB 656 AAATAGCCAGTGCCTTTGGGCTACCTGCATTCACTGAACATCGTTTATAGAGACTTAAAC 715
 QY 716 CAGAGAATATTTTGTGTAGATTACAGGGACACATTGCTCTTACTGATTTCCGACTCTGCA 775
 DB 716 CAGAGAATATTTTGTGTAGATTACAGGGACACATTGCTCTTACTGATTTCCGACTCTGCA 775
 QY 776 AGGAGAACATTTGAACACACAGACACAAATCCACCTTCTGTGGCAGCCGCGAGTATCTG 835
 DB 776 AGGAGAACATTTGAACACACAGACACAAATCCACCTTCTGTGGCAGCCGCGAGTATCTG 835
 QY 836 CACCTGAGTGTCTTCAAGACAGCCTTATGACAGGACTGTGGAATGCTGCTGCTGGGAG 895
 DB 836 CACCTGAGTGTCTTCAAGACAGCCTTATGACAGGACTGTGGAATGCTGCTGCTGGGAG 895
 QY 896 CTGCTTTGTATGAGATGCTGTATGGCTGCGCTTTTATAGCCGAAACACAGCTGAAA 955
 DB 896 CTGCTTTGTATGAGATGCTGTATGGCTGCGCTTTTATAGCCGAAACACAGCTGAAA 955
 QY 956 TGTACGACAAATTTCTGAACAAAGCCTTCTCAGCTGAACCAATATACAAATTCGCA 1015
 DB 956 TGTACGACAAATTTCTGAACAAAGCCTTCTCAGCTGAACCAATATACAAATTCGCA 1015
 QY 1016 GACACCTCTCGAGGCGCTCTGACAGAGCAGGACAAAGCGCTCGGGCCCAAGATG 1075
 DB 1016 GACACCTCTCGAGGCGCTCTGACAGAGCAGGACAAAGCGCTCGGGCCCAAGATG 1075
 QY 1076 ACTTATGAGATTAAGAGTCAATGCTTCTTCTTAAATTAACCTGGATGATCTCATTA 1135
 DB 1076 ACTTATGAGATTAAGAGTCAATGCTTCTTCTTAAATTAACCTGGATGATCTCATTA 1135
 QY 1136 ATAAGAAATTAATCTCCCTTTTAAACCAATGTGAGTGGGCCCAACGACTACGGGACT 1195
 DB 1136 ATAAGAAATTAATCTCCCTTTTAAACCAATGTGAGTGGGCCCAACGACTACGGGACT 1195
 QY 1196 TTGACCCCGAGTTTACCGAAGAGCCTGTCCTCCAACTCCATTGGCAAGTCCCTTGACAGCG 1255
 DB 1196 TTGACCCCGAGTTTACCGAAGAGCCTGTCCTCCAACTCCATTGGCAAGTCCCTTGACAGCG 1255
 QY 1256 TCCTCGTCAAGCGCTCAAGGAGCTGCGGAGGCTTTTCTAGGCTTTTCTTATGCGC 1315
 DB 1256 TCCTCGTCAAGCGCTCAAGGAGCTGCGGAGGCTTTTCTAGGCTTTTCTTATGCGC 1315
 QY 1316 CTCCTCAAGGACTTTTCTCTCTGA 1338
 DB 1316 CTCCTCAAGGACTTTTCTCTCTGA 1338

RESULT 7
 ABL70006
 ID ABL70006 standard; DNA; 2370 BP.
 XX
 XX ABL70006;
 AC
 XX
 DT 15-MAY-2002 (first entry)
 XX
 DE Pancreas cancer related gene sequence SEQ ID NO:8343.
 XX
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 XX gene; ds.
 XX

OS Homo sapiens.

XX WO200194629-A2.
XX 13-DEC-2001.
XX 30-MAY-2001; 2001WO-US10838.
XX 05-JUN-2000; 2000US-209473P.
XX 05-JUN-2000; 2000US-209531P.
XX 18-SEP-2000; 2000US-233133P.
XX 18-SEP-2000; 2000US-233617P.
XX 20-SEP-2000; 2000US-234009P.
XX 20-SEP-2000; 2000US-234034P.
XX 20-SEP-2000; 2000US-234052P.
XX 22-SEP-2000; 2000US-234509P.
XX 22-SEP-2000; 2000US-234567P.
XX 25-SEP-2000; 2000US-234923P.
XX 25-SEP-2000; 2000US-234924P.
XX 25-SEP-2000; 2000US-235077P.
XX 25-SEP-2000; 2000US-235082P.
XX 25-SEP-2000; 2000US-235134P.
XX 25-SEP-2000; 2000US-235280P.
XX 26-SEP-2000; 2000US-235637P.
XX 26-SEP-2000; 2000US-235638P.
XX 27-SEP-2000; 2000US-235711P.
XX 27-SEP-2000; 2000US-235720P.
XX 27-SEP-2000; 2000US-235740P.
XX 27-SEP-2000; 2000US-235840P.
XX 27-SEP-2000; 2000US-235863P.
XX 28-SEP-2000; 2000US-236028P.
XX 28-SEP-2000; 2000US-236032P.
XX 28-SEP-2000; 2000US-236033P.
XX 28-SEP-2000; 2000US-236034P.
XX 28-SEP-2000; 2000US-236109P.
XX 28-SEP-2000; 2000US-236111P.
XX 29-SEP-2000; 2000US-236842P.
XX 29-SEP-2000; 2000US-236891P.
XX 02-OCT-2000; 2000US-237172P.
XX 02-OCT-2000; 2000US-237173P.
XX 02-OCT-2000; 2000US-237278P.
XX 02-OCT-2000; 2000US-237294P.
XX 02-OCT-2000; 2000US-237295P.
XX 02-OCT-2000; 2000US-237316P.
XX 03-OCT-2000; 2000US-237425P.
XX 03-OCT-2000; 2000US-237598P.
XX 03-OCT-2000; 2000US-237604P.
XX 03-OCT-2000; 2000US-237606P.
XX 03-OCT-2000; 2000US-237608P.
XX 01-NOV-2000; 2000US-244867P.
XX 01-NOV-2000; 2000US-245084P.

(AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
XX Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.

PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -

XX Claim 1; SEQ ID 8343; 44pp; English.

XX The present invention describes a method (M1) for screening for an
XX anti-neoplastic agent. The method involves exposing cells to a chemical
XX agent to be tested for anti-neoplastic activity, determining a change in
XX expression of at least one gene (I) of a signature gene set, where (I)
XX comprises a sequence (S) selected from 8447 sequences (given in ABL61664
XX to ABL70110), or is at least 95% identical to (S), where a change in
XX expression is indicative of anti-neoplastic activity. (I) has cytostatic
XX activity and can be used in gene therapy. M1 can be used for screening
XX an anti-neoplastic agent, and can be used for producing a product which

CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumour.

XX Sequence 2370 BP; 636 A; 517 C; 513 G; 704 T; 0 other;

Query Match 91.0%; Score 1218.2; DB 24; Length 2370;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	116	TGCTTTTCATGAAGCAGAGGAGGATGGGTCTCAACGACTTTATTCAGAGATTGCCAATA	175
DB	116	TGCTTTTCATGAAGCAGAGGAGGATGGGTCTCAACGACTTTATTCAGAGATTGCCAATA	175
QY	176	ACTCTTATGATGCAACACACCTGGAAGTTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG	235
DB	176	ACTCTTATGATGCAACACACCTGGAAGTTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG	235
QY	236	AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCCAAGTCTTCTCAGCAAAATCAACC	295
DB	236	AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCCAAGTCTTCTCAGCAAAATCAACC	295
QY	296	TTGGCCCGTCTGCTCAATCTCATGTAACCATCTGACTTTTCACTTTCTTGAAGTATCG	355
DB	296	TTGGCCCGTCTGCTCAATCTCATGTAACCATCTGACTTTTCACTTTCTTGAAGTATCG	355
QY	356	GAAAGGGCAGTTTGGAAAGGTTCTTCTAGCAAGACACAAAGGAGAGAGTGTCTCTATG	415
DB	356	GAAAGGGCAGTTTGGAAAGGTTCTTCTAGCAAGACACAAAGGAGAGAGTGTCTCTATG	415
QY	416	CAGTCAAAAGTTTACAGAAAGAAAGCAATCTGAAAGAAAGAGAGAGATATTATGT	475
DB	416	CAGTCAAAAGTTTACAGAAAGAAAGCAATCTGAAAGAAAGAGAGAGATATTATGT	475
QY	476	CGGAGCGGAATGTTCTGTTGAAGAAATGTCAGCAACCCCTTCTCTGGTGGGCTTCACTTCT	535
DB	476	CGGAGCGGAATGTTCTGTTGAAGAAATGTCAGCAACCCCTTCTCTGGTGGGCTTCACTTCT	535
QY	536	CTTTCCAGACTGCTGACAAATGTTACTTTGTCTCTAGACTACATTAATGTTGGAGAGTTGT	595
DB	536	CTTTCCAGACTGCTGACAAATGTTACTTTGTCTCTAGACTACATTAATGTTGGAGAGTTGT	595
QY	596	TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCAACCGGCTCTTTTCTATGCTGCTG	655
DB	596	TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCAACCGGCTCTTTTCTATGCTGCTG	655
QY	656	AAATAGCCAGTCTGGGCTACCTGCAATCTCACTGACATCGTTTATAGAGCTTAAAC	715
DB	656	AAATAGCCAGTCTGGGCTACCTGCAATCTCACTGACATCGTTTATAGAGCTTAAAC	715
QY	716	CAGAGAAATTTTGTCTAGATTTCAGGGACACATCTCTTACTGACTTCGGACTCTGCA	775
DB	716	CAGAGAAATTTTGTCTAGATTTCAGGGACACATCTCTTACTGACTTCGGACTCTGCA	775
QY	776	AGGAGAAATTTGAAACAAACAGCACAACATCCACTTCTGTTGGCAGCCGGAGTATCTCG	835
DB	776	AGGAGAAATTTGAAACAAACAGCACAACATCCACTTCTGTTGGCAGCCGGAGTATCTCG	835
QY	836	CACCTGAGTCTTATAGAGTCTGATGGCTGCGGCTCTTTTATAGCCGAAACACAGCTGAAA	895
DB	836	CACCTGAGTCTTATAGAGTCTGATGGCTGCGGCTCTTTTATAGCCGAAACACAGCTGAAA	895
QY	896	CTGCTTGTATGAGTCTGATGGCTGCGGCTCTTTTATAGCCGAAACACAGCTGAAA	955
DB	896	CTGCTTGTATGAGTCTGATGGCTGCGGCTCTTTTATAGCCGAAACACAGCTGAAA	955
QY	956	TGTACGACAACTTCTGAAACAGCCCTCTCAGCTGAAACCAAAATATTACAAATTCGCAA	1015
DB	956	TGTACGACAACTTCTGAAACAGCCCTCTCAGCTGAAACCAAAATATTACAAATTCGCAA	1015

Db 956 TGTACGACCAATTTCTGACAGCGCTCTCAGCTGAACCAATATTACAAATTCGCCAA 1015
 Qy 1016 GACACCTCTGGAGGGCTCTCTGAGAGGACAGACAAAGCGCTCGGGCCCAAGGATG 1075
 Db 1016 GACACCTCTGGAGGGCTCTCTGAGAGGACAGACAAAGCGCTCGGGCCCAAGGATG 1075
 Qy 1076 ACTTCATGGAGATTAAAGATCATGTCTTCTTCTTAAATTAAGTGGATGATCTCATTA 1135
 Db 1076 ACTTCATGGAGATTAAAGATCATGTCTTCTTCTTAAATTAAGTGGATGATCTCATTA 1135
 Qy 1136 ATAAGAAGATTACTCCCGCTTTTAAACCAATGTAGTGGGCCCAAGCGCTACGGCACT 1195
 Db 1136 ATAAGAAGATTACTCCCGCTTTTAAACCAATGTAGTGGGCCCAAGCGCTACGGCACT 1195
 Qy 1196 TTGACCCCGAGTTTACCGAAGAGCTGTGCCCACTCCATTTGGCAAGTCCCTGACAGCG 1255
 Db 1196 TTGACCCCGAGTTTACCGAAGAGCTGTGCCCACTCCATTTGGCAAGTCCCTGACAGCG 1255
 Qy 1256 TCCTGTCACAGCCAGGCTCAGGAAGCTGCGAGGCTTTCTTAGGCTTTTCTATGCGC 1315
 Db 1256 TCCTGTCACAGCCAGGCTCAGGAAGCTGCGAGGCTTTCTTAGGCTTTTCTATGCGC 1315
 Qy 1316 CTCCACGGACTCTTTCTCTGA 1338
 Db 1316 CTCCACGGACTCTTTCTCTGA 1338

RESULT 8

AZ33647
 ID AZ33647 standard; cDNA; 2281 BP.
 AC AZ33647;
 DT 08-DEC-1999 (first entry)
 DE Human breast tumour-associated EST 37.
 XX
 KW Expressed sequence tag; EST; human; breast; cancer; gene therapy;
 KW treatment; tumour; cytostatic; medicament; ss.
 XX
 OS Homo sapiens.
 XX
 PN DEL9813839-A1.
 XX
 PD 23-SEP-1999.
 XX
 PF 20-MAR-1998; 98DE-1013839.
 XX
 PR 20-MAR-1998; 98DE-1013839.
 XX
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX
 PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
 XX
 DR WPI; 1999-528981/45.
 DR P-PSDB; AAY48573.
 XX
 PT Human nucleic acid sequences and protein products from tumor breast
 PT tissue, useful for breast cancer therapy -
 XX
 PS Claim 1a; 116-117; 180pp; German.
 XX
 CC This invention describes novel human nucleic acid sequences from tumor
 CC breast tissue which have cytostatic activity. The nucleic acid sequences
 CC can be used to produce and isolate full-length gene sequences. They can
 CC be used to express proteins, which can be used as tools to find an
 CC activity against breast cancer. The sequences can be used in sense or
 CC antisense form. They are especially useful for medicaments for gene
 CC therapy to treat breast cancer. AA233611-248617 represents expressed
 CC sequence tags described in the method of the invention.
 XX
 SQ Sequence 2281 BP; 601 A; 498 C; 494 G; 688 T; 0 other;

Query Match 85.5%; Score 1144; DB 20; Length 2281;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 195 CCCTGAAGTTCAGTCCCATCTTGAAGATCTCCCAACCTCAGGAGCCTGAGCTTATGAATGC 254
 Db 95 CCCTGAAGTTCAGTCCCATCTTGAAGATCTCCCAACCTCAGGAGCCTGAGCTTATGAATGC 154
 Qy 255 CAACCCCTTCTCTCCACCAAGTCTTCTCAGCAAAATCAACCTTGGCCCGCTGCTCCCAATCC 314
 Db 155 CAACCCCTTCTCTCCACCAAGTCTTCTCAGCAAAATCAACCTTGGCCCGCTGCTCCCAATCC 214
 Qy 315 TCATGTAAACCATCTGACTTTTCTTCACTTCTTGAAGTATCGGAAGCGCATTTTGGAAA 374
 Db 215 TCATGTAAACCATCTGACTTTTCTTCACTTCTTGAAGTATCGGAAGCGCATTTTGGAAA 274
 Qy 375 GGTTCCTTCTAGCAAGACACAAGGACAGAAGTGTCTATGCAAGTCAAAAGTCTTACAGAA 434
 Db 275 GGTTCCTTCTAGCAAGACACAAGGACAGAAGTGTCTATGCAAGTCAAAAGTCTTACAGAA 334
 Qy 435 GAAAGCAATCTCTGAAAAGAAAGAGGAGAGCATATTATGTCGGAGCGGAATGTTCTGTT 494
 Db 335 GAAAGCAATCTCTGAAAAGAAAGAGGAGAGCATATTATGTCGGAGCGGAATGTTCTGTT 394
 Qy 495 GAAAGATGTAAGCAACCTTTCTGTGGGCTTCTCACTTCTTTCAGACTGCTGACAA 554
 Db 395 GAAAGATGTAAGCAACCTTTCTGTGGGCTTCTCACTTCTTTCAGACTGCTGACAA 454
 Qy 555 ATTGTACTTGTCTAGACTACATTAATGTTGGAGAGTGTCTTACCATCTCCAGAGGA 614
 Db 455 ATTGTACTTGTCTAGACTACATTAATGTTGGAGAGTGTCTTACCATCTCCAGAGGA 514
 Qy 615 ACGCTGCTTCTGGAACACCGGCTCGTTTCTATGCTGTGTAATAGCAAGTGCCTTGGG 674
 Db 515 ACGCTGCTTCTGGAACACCGGCTCGTTTCTATGCTGTGTAATAGCAAGTGCCTTGGG 574
 Qy 675 CTACCTGCAATCTGAAACATCTGTTATAGACTTTAAACACAGAGATATTTTGTGAGA 734
 Db 575 CTACCTGCAATCTGAAACATCTGTTATAGACTTTAAACACAGAGATATTTTGTGAGA 634
 Qy 735 TTCACAGGACACATTTGCTTACTGACTTCGAGCTCTGCAAGGAGAACTTGAACACAA 794
 Db 635 TTCACAGGACACATTTGCTTACTGACTTCGAGCTCTGCAAGGAGAACTTGAACACAA 694
 Qy 795 CAGCACAAATCCACCTTCTGTGGCACGCGGAGTATCTCGACCTGAGGTGTTCTATAA 854
 Db 695 CAGCACAAATCCACCTTCTGTGGCACGCGGAGTATCTCGACCTGAGGTGTTCTATAA 754
 Qy 855 GCAGCCTTATGACAGACTGTGGAATGTTGGTGGCTGGGAGCTGTCTTGTATGAGATGCT 914
 Db 755 GCAGCCTTATGACAGACTGTGGAATGTTGGTGGCTGGGAGCTGTCTTGTATGAGATGCT 814
 Qy 915 GTATGGCCTGCGGCTTTTATAGCCGAAACACAGCTGAAATGTAGCAACATTTCTGAA 974
 Db 815 GTATGGCCTGCGGCTTTTATAGCCGAAACACAGCTGAAATGTAGCAACATTTCTGAA 874
 Qy 975 CRAAGCTCTCCAGCTGAAACCAATATTACAAATTCGCAAGACACCTCTCTGAGGCGCT 1034
 Db 875 CRAAGCTCTCCAGCTGAAACCAATATTACAAATTCGCAAGACACCTCTCTGAGGCGCT 934
 Qy 1035 CCTGCAGAGGACAGACAAAGCGCTCGGGGCCAAGGATGACTTTCATGAGATTAAAGAG 1094
 Db 935 CCTGCAGAGGACAGACAAAGCGCTCGGGGCCAAGGATGACTTTCATGAGATTAAAGAG 994
 Qy 1095 TCATGTCTTCTTCTTCTTAACTTGGATGATCTCATTAATAAGAGATTACTCCCC 1154
 Db 995 TCATGTCTTCTTCTTCTTAACTTGGATGATCTCATTAATAAGAGATTACTCCCC 1054
 Qy 1155 TTTTAAACCAAAATGTCAGTGGGCCCAACGACCTTACGGCACTTTTGACCCCGAGTTTACCGA 1214
 Db 1055 TTTTAAACCAAAATGTCAGTGGGCCCAACGACCTTACGGCACTTTTGACCCCGAGTTTACCGA 1114
 Qy 1215 AGAGCCTGTCCCCAACTTCCATTGGCAAGTCCCTGTGACAGCGTCTCTGTACAGCCAGCGT 1274

Db 1115 AGAGCTGTCCCAACTCCATTGGCAGTCCCTGACAGAGTCTCTGTCACAGCCAGCGT 1174
 Qy 1275 CAAGGAAGCTGCGAGAGCTTTCTTAGGCTTTTCTATGCGCTCCCAAGGACTCTTTCTT 1334
 Db 1175 CAAGGAAGCTGCGAGAGCTTTCTTAGGCTTTTCTATGCGCTCCCAAGGACTCTTTCTT 1234
 Qy 1335 CTGA 1338
 Db 1235 CTGA 1238

RESULT 9

AAA46592

ID AAA46592 standard; DNA; 2365 BP.

XX

AC AAA46592;

XX

DT 25-SEP-2000 (first entry)

XX

DE DNA encoding a rat serum and glucocorticoid induced protein kinase.

XX

KW Protein kinase; Pkh1; Pkh2; Ypk1; Yrk2; protein kinase B-alpha;
 KW serum and glucocorticoid induced protein kinase; SGK; PKBalpha;
 KW 3-phosphoinositide-dependent protein kinase-1; PDK1; fungal infection;
 KW thrush; cancer; diabetes; obesity; antifungal; Candida infection; ss.
 XX

OS Rattus sp.

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FH Key

FT CDS

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CC (Ypk1 or Yrk2) can be used as an antifungal agent to treat Candida
 CC infections, e.g. thrush.

XX Sequence 2365 BP; 591 A; 580 C; 518 G; 676 T; 0 other;

SQ Query Match 73.5%; Score 983; DB 21; Length 2365;

Best Local Similarity 88.3%; Pred. No. 7.3e-280;

Matches 1080; Conservative 0; Mismatches 140; Indels 3; Gaps 1;

Qy 116 TGGCTTTTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTTATTCAGAGATTGCCAATA 175

Db 69 TCGCTTTTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTTATTCAGAGATTGCCAATA 128

Qy 176 ACTCTTATGATGCAAAACACCTCTGAAGTTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235

Db 129 ACTCTTATGATGCAAAACACCTCTGAAGTTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 188

Qy 236 AGCTGAGCTTATGAATGCCAACCCCTTCTCCCAAGTCTCTTCAGCAAAATCAACC 295

Db 189 AGCTGAGCTTATGAATGCCAACCCCTTCTCCCAAGTCTCTTCAGCAAAATCAACC 248

Qy 296 TTGGCCCGTCTCCATCTCTGCTAAACCATCTGACTTTTCACTTTTGAAGTCTATCG 355

Db 249 TTGGCCCGTCTCCATCTCTGCTAAACCATCTGACTTTTCACTTTTGAAGTCTATCG 308

Qy 356 GAAAGGCGAGTTTGGAAAGGTTTCTTAGCAAGACACAAGGCGAGAAAGTCTTCTATG 415

Db 309 GAAAGGCGAGTTTGGAAAGGTTTCTTAGCAAGGCGAGAAAGTCTTCTATG 368

Qy 416 CAGTCAAAAGTTTACAGAAAGCAATCTCTGAAAGAAAGAGGAGAGCAATATATGT 475

Db 369 CAGTCAAAAGTTTACAGAAAGCAATCTCTGAAAGAAAGAGGAGAGCAATATATGT 428

Qy 476 CGGAGCGGAATGTTCTGTTGAAGATGTGAAGCACCCTTTCTGTTGGGCTTCACTTCT 535

Db 429 CGGAGCGGAATGTTCTGTTGAAGATGTGAAGCACCCTTTCTGTTGGGCTTCACTTCT 488

Qy 536 CTTTCCAGACTGCTGACAAATTTGTTCTCTAGACTACATTAATGTTGAGAGAGTGT 595

Db 489 CTTTCCAGACTGCTGACAAATTTGTTCTCTAGACTACATTAATGTTGAGAGAGTGT 548

Qy 596 TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCCGCGCTCTTCTATGCTGCTG 655

Db 549 TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCCGCGCTCTTCTATGCTGCTG 608

Qy 656 AATAGCCAGTCCCTTGGGCTACCTGCTTCTGAGACATCTTTTATAGAGACTTAAAC 715

Db 609 AATAGCCAGTCCCTTGGGCTACCTGCTTCTGAGACATCTTTTATAGAGACTTAAAC 668

Qy 716 CAGAGAAATTTTGTCTAGATTTCAGAGGACACATTTCTCTTACTGACTTCGGACTCTGCA 775

Db 669 CAGAGAAATTTTGTCTAGATTTCAGAGGACACATTTCTCTTACTGACTTCGGACTCTGCA 728

Qy 776 AGGAGAAATTTGAAACACACAGCAAAATCCACCTTCTGTTGGCAGCGCGAGTATCTCG 835

Db 729 AGGAGAAATTTGAAACACACAGCAAAATCCACCTTCTGTTGGCAGCGCGAGTATCTCG 788

Qy 836 CACCTGAGTGTCTTATAGCAGCCTTATGACAGGACTGTGGACTGGTGGCTGGGAG 895

Db 789 CACCTGAGTGTCTTATAGCAGCCTTATGACAGGACTGTGGACTGGTGGCTGGGAG 848

Qy 896 CTGCTTTGTATGAGATGCTGTATGGCTGCTGGCTTTTATAGCCGAAACACAGCTGAAA 955

Db 849 CTGCTTTGTATGAGATGCTGTATGGCTGCTGGCTTTTATAGCCGAAACACAGCTGAAA 908

Qy 956 TGTACGACAAATTTGAAACACAGCAAAATCCAGCTGAAACCAATATATACAAATTCGCAA 1015

Db 909 TGTATGACAAATTTGAAACACAGCAAAATCCAGCTGAAACCAATATATACAAATTCGCAA 965

Qy 1016 GACACCTCTGGAGGCTCTTCTGCAAGGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 1075

Db 966 GACACCTCTGGAGGCTCTTCTGCAAGGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 1025

Disclosure; Fig 12; 155pp; English.

The present sequence encodes a rat serum and glucocorticoid induced protein kinase (SGK). The specification describes a screening method to identify a compound which modulates the activity of protein kinases from different sources, using host yeast cells. The method is used to identify a compound which modulates (inhibits) the activity of a protein kinase. Pkh1 or Pkh2 phosphorylate and activate Ypk1, Yrk2, SGK or protein kinase B-alpha (PKBalpha). 3-phosphoinositide-dependent protein kinase-1 (PDK1) is used to phosphorylate and activate Ypk1 and Yrk2 or SGK but not PKBalpha or p70S6 kinase. Compounds identified by the methods are used to treat fungal infections e.g. thrush, and to treat cancer. To treat cancer, the compounds inhibit PKB, PDK1 or the activation of PKB by PDK1. Compounds which activate PKB or PDK1 can be used in the treatment of diabetes or obesity, and compounds which inhibit a fungal functional homologue of PDK1 (Pkh1 or Pkh2) or SGK

Db 1045 GGCACCTCTGGAGGCTCTCTGAGAGGACCGGACCAAGAGGCTGGGTGCAAGGATG 1104
 Qy 1076 ACTTCAGGAGATTAAAGATCATGCTTCTCTCTCTTAATTAAGTGGATGATCTCATTA 1135
 Db 1105 ACTTTATGGAGATTAAAGATCATATTTCTCTCTTTAATTAAGTGGATGATCTCATCA 1164
 Qy 1136 ATAAGAAGATTACTCCCTCTTTAAACCAATGTGAGTGGGCCCAAGCACTACGGCACT 1195
 Db 1165 ATAAGAAGATTACACCCCAATTTAAACCAATGTGAGTGGGCCCAAGCACTTCGGCACT 1224
 Qy 1196 TTGACCCCGAGTTTACCAAGAGAGCTGTCCCAACTCCATTGGCAAGTCCCTCGACAGCG 1255
 Db 1225 TCGATCCGAGTTTACCGAGAGCGGTCCCAAGTCCATCGCAGGTCCCTCGACAGCA 1284
 Qy 1256 TCCTCGTCAGACCGAGCGTCAAGAAAGTGGCGAGGCTTTCCTAGGCTTTCTCTATGCGC 1315
 Db 1285 TCCTGTGTACGGCCAGTGTGAAGGAAGCAGCAGAGAGCTTCTCTCGGCTTCTCTATGCGC 1344
 Qy 1316 CTCACCGAGCTCTTCTCTCTGA 1338
 Db 1345 CTCTGTGGATTCTTCTCTCTGA 1367

RESULT 11

AAS44987
 ID AAS44987 standard; cDNA; 1366 BP.

XX AAS44987;

DT 18-DEC-2001 (first entry)

XX cDNA encoding novel human secretory protein, Seq ID No 68.

XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW myotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen; ss.

XX Homo sapiens.

XX W0200166689-A2.

XX 13-SEP-2001.

XX 05-MAR-2001; 2001WO-US04942.

XX 07-MAR-2000; 2000US-0519705.

XX 19-MAY-2000; 2000US-0574454.

XX 17-JUN-2000; 2000US-0596193.

XX 14-JUL-2000; 2000US-0616847.

XX 19-SEP-2000; 2000US-0665363.

XX 20-OCT-2000; 2000US-0693267.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren P, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

XX WPI; 2001-589934/66.

XX P-PSDB; AAU28087.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -

XX Claim 1; SEQ ID No 68; 107pp; English.

XX

CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms, of
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAS44920-AAS45295 represent novel human secreted protein
 CC coding sequences of the invention.

XX SQ Sequence 1366 BP; 331 A; 374 C; 377 G; 284 T; 0 other;

Query Match 39.4%; Score 527.2; DB 22; Length 1366;
 Best Local Similarity 69.5%; Pred. No. 3.5e-145;

Matches 734; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

Qy 261 TTCTCTCCACCAAGTCTTCTCAGCAATCAACCTTGGCCCTCTCCAACTCCTCATGC 320

Db 213 TCCACAGCCCTCCAGGCGCAATGGGAACATCAACCTGGGGCTTTCAGCCAACTCAATGC 272

Qy 321 TAAACCATCTGACTTTCCTTCTTGAAGTATCGGAAGGCGAGTTTGGAAAGCTTCT 380

Db 273 CCAGCCCGGAGCTTCGACTTCTCAAGTCTCGGCAAGGGAAGTACGGGAAGTCTCT 332

Qy 381 TCTAGCAAGACACAAGGCGAGAGAGTGTCTATGCAGTCAAAAGTTTACAGAGAAAGC 440

Db 333 ACTGGCCCAAGCGCAAGTCTGTATGGGCGTTCTATGCAGTGAAGTACTACAGAAAAGTC 392

Qy 441 AATCTTGAAAAAGAAAGAGAGAGAGCAATATTATGTCGGAGCGGAATGTTCTGTGAAGAA 500

Db 393 CATCTTAAAGAAAGAAAGAGAGAGAGCAATCATATGGCAGAGCGCAGTGTCTTCTGAAGAA 452

Qy 501 TGTGAAGCAACCTTTCTCTGGTGGCCCTTCACTTCTTCTTCCAGACTGCTGACAAATGTA 560

Db 453 CGTGGGCAACCCCTTCTCTGGGCGCTGCGCTACTCTTCCAGACACCTTGAAGGCTCTA 512

Qy 561 CTTTGTCTTAGACTACATTAATGTTGGAGAGTGTGTTCTACCATCTCCAGAGGGAAGCTG 620

Db 513 CTTCGTGCTCGACTATGTCTCAACGGGGGAGAGCTCTTCTTCCACCTCGAGGGGAGCGCG 572

Qy 621 CTTCCTGGAAACCAACCGGCTCGTTTCTATGCTGCTGAAATAGCCAGTGCCTTGGGCTACCT 680

Db 573 GTTCTCTGGAGCCCGGGCCAGGTTCTACGCTGTGAGGTGGCCAGCGCCATTGGCTACCT 632

Qy 681 GCATTCACCTGACATCGTTTATAGACACTTAAACCCAGAGAAATATTTTGTAGATTACCA 740

Db 633 GCACTCCCTCAACATCATTTACAGGGATCTGAAACCCAGAGAAACATTTCTTTGACTGCCA 692

Qy 741 GGGACACATTGTCTTACTGACTTTCGAGCTCTGCAAGGAGAAACATTGAACACACAGCAC 800

Db 693 GGGACAGTGGTCTGACGAGATTGTCCTCTGCAAGGAAGGTGTAGAGCTGAAGACAC 752
 Qy 801 AACATCCACCTTCTGTGCGACCGCGAGTATCTGACACCTGAGGTGCTTCATAGCAGCC 860
 Db 753 CACATCCACATCTGTGTACCTGCTGAGTACTTGGCACCTGAAGTCTTCGGAAGAGCC 812
 Qy 861 TTATGACAGACTGTGACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 920
 Db 813 TTATGATCGACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 872
 Qy 921 CCTGCCCTTTTATAGCCGAAACACAGCTGAATCTGACACACATCTGTAACAGCC 980
 Db 873 CCTGCCCTTTTACAGCCAAAGATGTATCCAGATGTATGAGAACATCTGACACAGCC 932
 Qy 981 TCTCCAGCTGAACCAATATTACAAATTCGCAAGACACCTCTGAGGCGCTCTCTGCA 1040
 Db 933 GCTACAGATCCCGAGCGCGACAGTGGCGCTGTGACCTCTGCAAGCTTCTCCA 992
 Qy 1041 GAAGGACAGACAAAGCGGTGCGGGCCAAAGGATGACTTCATGAGAGATTAGAGTCAATG 1100
 Db 993 CAAGGACAGAGCGAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1052
 Qy 1101 CTCTCTCTCTTAATTAAGTGGGATGATCTCATTAAGAAGATTACTCCCTTTTAA 1160
 Db 1053 ATTCTTCAGCCCCATAAAGTGGGATGACCTGTATACCAAGAGGCTAACTCCACCTTCAA 1112
 Qy 1161 CCCAAATGTAGTGGGCGCAAGCAGCTACGCGACTTTGACCCCGAGTTTACCGAAGAGCC 1220
 Db 1113 CCCAAATGTAGCAGGACTGCTGACTTGAAGCATTTTGACCCAGATTTACCCAGGAGC 1172
 Qy 1221 TGTCCCAACTCCATTTGGCAAGTCCCTGACAGCGTCTCTGTCACAGCCAGCGTCAAGGA 1280
 Db 1173 TGTGTCCAAAGTCCATTTGGTGTACCCCTGACACTGT-----GGCCAGCAGCTCTGG 1223
 Qy 1281 AGTGGCGAGGCTTCTTAGGCTTTTCTATGCGCC 1316
 Db 1224 GGCTCAAGTGCATTCCTGGGATTTTCTTATGCGCC 1259

RESULT 12
 AAF44737
 ID AAF44737 standard; cDNA; 1812 BP.

XX AAF44737;

DT 27-MAR-2001 (first entry)

XX Novel protein kinase cDNA, SEQ ID NO: 118.

XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiac; renal; antiinflammatory; antiaesthetic;
 KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.

OS Homo sapiens.

XX WO200073469-A2.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US14842.

XX 28-MAY-1999; 99US-0136503.

XX (SUGEN-) SUGEN INC.

XX Plowman GD, Martinez R, Whyte D, Sudersanam S;

XX WPI; 2001-032161/04.

DR P-PSDB; AAB65708.

XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers -
 XX Disclosure; Fig 2; 31opp; English.

XX The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomyopathies, strokes, renal failure,
 CC oxidative-stress related disorders, chronic inflammatory bowel disease,
 CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
 CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
 CC reproductive disorders.

XX SQ Sequence 1812 BP; 461 A; 470 C; 470 G; 411 T; 0 other;

Query Match 39.4%; Score 527.2; DB 22; Length 1812;
 Best Local Similarity 69.5%; Pred. No. 4.1e-145;
 Matches 734; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

Qy 261 TTCTCTCCACCAAGTCTTCTCAGCAATCAACCTTGGCCCTGCTCCAAATCTCATGC 320
 Db 117 TCCACAGCCCTCCAGGCGCAATGGGAACATCAACCTGGGCGCTTCAGCCAACTATGC 176
 Qy 321 TAAACCATCTGACTTTCATCTTGAAGTATCGGAAGGAGGAGTTCGGAAGGTTCT 380
 Db 177 CCAGCCCGAGGACTTCGACTTCTCAAGTCACTCGGCAAGGGAAGTACCGGAGGTCCT 236
 Qy 381 TCTAGCAAGACACAAGGAGGAAGTGTCTATGAGTCAAGTCTTACAGAGGAAGAC 440
 Db 237 ACTGGCCNAGCGAAGTCTGATGGGCGTCTATGAGTCAAGTACTACAGAAAAGTC 296
 Qy 441 AATCTCTGAAAAGAAAGAGAGAGCATATATGTCGGAGCGGAATGTTCTGTGAAGAA 500
 Db 297 CATCTTAAAGAAAGAGAGAGAGAGCAGATCATGCGAGAGCGCAGTGTCTTCTGAAGAA 356
 Qy 501 TGTGAAGACCCCTTCTGTTGGGCGCTTCACTTCTCTTCCAGACTGCTGACAAATTGTA 560
 Db 357 CGTGGCGCACCCCTTCTGTTGGGCGCTGCGCTACTCTCTCCAGACACTGAGAGCTCTA 416
 Qy 561 CTTTGTCTAGACTACATTAATGTCGAGAGTGTGTTCTACCATCTCCAGAGGGAACGCTG 620
 Db 417 CTTCTGTCTCGACTATGTCACCGGGGAGAGTCTTCTTCCACTGCGAGGAGCGCCG 476
 Qy 621 CTTCTCTGGAACACCGGCGCTCGTTTCTATGCTGCTGAAATAGCCAGTGCCTTGGGCTACCT 680
 Db 477 GTTCTCTGGAGCCCGGCGCAGGTTCTACGCTGCTGAGGTGCGCAGCGCATTTGCTACCT 536
 Qy 681 GCATTCTGAAACATCGTTTATAGAGACTTAAACACAGAGAATATTTTGTAGATTACA 740
 Db 537 GCACCTCCCTCAACATCATTTACAGGGATCTGAAACACAGAGAATCTCTCTTGGACTGCCA 596
 Qy 741 GGGACACATGTCTTACTGACTTCGAGCTCTCAAGGAGAACATTGAACACACACACAC 800
 Db 597 GGGACACGTGGTGTGACCGATTTTGGCCCTCTGCAAGGAAGGTGTAGAGCCTGAAGACAC 656
 Qy 801 AACATCCACCTTCTGTGGCACCGCGGAGTATCTCGACCTCGAGTGTCTTCATAGCAGCC 860
 Db 657 CACATCCACATTTCTGTGTACCCCTGAGTACTTGGCAGCTGAGTGTCTTCGGAAGAGCC 716
 Qy 861 TTATGACAGACTGTGTGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 920

Db 717 TTATGATCGAGCAGTGACTGGTGGTCTTTGGGGCAGTCTCTACGAGATGCTCCATGG 776
Qy 921 CCTGCCGCCCTTTTATAGCGCAACACAGCTGAAATGTACGACAACTTCTGAACAAGCC 980
Db 777 CCTGCCGCCCTTTTACAGCCAAAGATGTATCCAGATGTATGAGAACATTTCTGACCAGCC 836
Qy 981 TCTCCAGCTGAAACCAATATTACAAATTTCCGAAGACACCTCTCTGAGGGCCTCTGCA 1040
Db 837 GCTACAGATCCCGAGCGCCGACAGTGGCGCTGTGACCTCTCTGCAAGCCTTCTCCA 896
Qy 1041 GAAGGACAGCAAAAGCGCTCGGGGCAAGGATGACTTCTATGAGATTAAAGATCATGT 1100
Db 897 CAAGGACAGGAGCGGCTGGGCTCCAAAGCAGAGCTTTCTTGAGATTAAAGACCATGT 956
Qy 1101 CTCTCTCTCTTAATTAACCTGGGATGATCTCAATTAAGAAGATTACTCCCTTTTAA 1160
Db 957 ATTCTTTCAGCCCACTAACTGGGATGACCTGTACCAAGAGGCTAACTCCACCTTCAA 1016
Qy 1161 CCCAAATGTGAGTGGGCGCCCAACGACCTACGCGACTTTGACCCGAGTTTACCGAAGAGCC 1220
Db 1017 CCCAAATGTGACAGGACCTGCTGACTTGAAGCATTTTGACCCAGAGTTTACCCAGGAAGC 1076
Qy 1221 TGTCCTCCCACTCAATGGGAAGTCCCTGACAGAGGCTCTCGTCACAGCCAGCGTCAAGGA 1280
Db 1077 TGTGTCCAAGTCCATTGGCTGTACCCCTGACACTGT-----GGCCAGCAGCTCTGG 1127
Qy 1281 AGCTGCCGAGGCTTTCTAGGCTTTTCTATGGGCC 1316
Db 1128 GGCCTCAAGTGCATTCTCTGGGATTTCTTATGGGCC 1163

RESULT 13

AAD36141
ID AAD36141 standard; DNA; 1812 BP.
XX AAD36141;
XX 09-AUG-2002 (first entry)
XX Human serum and glucocorticoid-induced protein kinase, SGK2-alpha gene.
XX Human; cytostatic; antisense gene therapy; screening; protein kinase;
KW cancer; liver; colon; tumour; inflammation; arthritic synovium; gene;
KW serum and glucocorticoid-induced protein kinase; SGK2-alpha; enzyme; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 88..1191
FT /*tag= a
FT /product= "Human SGK2-alpha protein"
XX
PN W0200224947-A2.
XX 28-MAR-2002.
XX 20-SEP-2001; 2001WO-IB02237.
XX 20-SEP-2000; 2000US-233999P.
PR 02-OCT-2000; 2000US-237419P.
PR 02-OCT-2000; 2000US-237423P.
PR 04-OCT-2000; 2000US-238558P.
PR 10-MAY-2001; 2001US-290555P.
XX (KINE-) KINETEK PHARM INC.
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Yoganathan T, Delaney AD;
XX WPI; 2002-394145/42.
DR P-PSDB; AAE22765.
XX
XX Diagnosing cancer, comprises determining the upregulation of expression

PT of a nucleic acid sequence encoding a protein kinase or upregulation of
PT expression of the protein kinase, in the cancer
XX Claim 16; Page 65-66; 87pp; English.
XX The invention relates to a method for screening biologically active agent
CC that modulates cancer associated protein kinase function. The invention
CC also relates to a method for diagnosing cancer comprising determining the
CC upregulation of expression of a nucleic acid sequence encoding a protein
CC kinase. The method is useful for diagnosing cancer. A protein kinase is
CC useful for screening biological agents that modulate cancer associated
CC protein kinase function. Downregulating the activity of protein kinase is
CC useful for inhibiting the growth of a cancer cell, e.g. liver or colon
CC cancer. A nucleic acid encoding protein kinase is useful to screen biopsy
CC derived tumours and inflammatory samples such as arthritic synovium, for
CC amplified DNA in the cell or increased expression of corresponding mRNA
CC or protein and is also useful to detect differences in expression levels
CC such as molecular weight, amino acid and nucleotide sequences between the
CC two cells. The present sequence is human serum and glucocorticoid-induced
CC protein kinase, SGK2-alpha gene.
XX
SQ Sequence 1812 BP; 461 A; 470 C; 470 G; 411 T; 0 other;

Query Match 39.4%; Score 527.2; DB 24; Length 1812;
Best Local Similarity 69.5%; Pred. No. 4.1e-145;
Matches 734; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

Qy 261 TTCTCTCTCCACCAAGTCTTCTCAGCAATCAACCTTGGCCGCTGCTCCAAATCCTCATGC 320
Db 117 TCACAGCCCTCCAGGGCAATGGGAACATCAACCTGGGGCCTTCAGCCAAACCAATGC 176
Qy 321 TAAACCATCTGACTTTTCACTTTTGAAGTGTATCGGAAGGCGAGTTTGGAAAGTTCT 380
Db 177 CCAGCCCAAGGACTTCGACTTCTCAAGTATCGGCNAAGGAAGTACGGGAAGTCTCT 236
Qy 381 TCTAGCAAGACACAAGGCAAGAAAGTGTCTATGCAAGTCAAAAGTTTTCAGAAAGAAC 440
Db 237 ACTGGCCAAAGCGCAAGTCTGATGGGCGTTCTATGCAAGTGAAGGTACTACAGAAAAGTC 296
Qy 441 AATCCTGAAAGAAAGAGAGAGAGCATATTATGTCGGAGCGGAATTTCTGTAGAGAA 500
Db 297 CATCTTTAAAGAAAG 356
Qy 501 TGTGAAGACCCCTTCTCTGGTGGCTTCACTTCTCTTCCAGACTGCTGACAAATGTGA 560
Db 357 CGTGGCGCACCCCTTCTCTGGTGGCTTCTCTTCCAGACTGCTGAGAGAGTCTTA 416
Qy 561 CTTTGTCTAGACTACATTAATGGTGGAGAGTTGTTCTACCATCTCCAGAGGAAAGCTG 620
Db 417 CTTCTGTCTGACTATGTCAACGGGGGAGAGTCTTCTTCCACCTGCAGCGGAGCGCG 476
Qy 621 CTTCTGTGAACACAGGGCTCGTTTCTATGCTGTGAATAGCCAGTCCCTTGGGCTACCT 680
Db 477 GTTCTGTGAGAGCCCGGGCCAGGTTCTACGCTGTGAGGTGGCCAGCCATTGGCTACCT 536
Qy 681 GCATTCACTGAACATCGTTTATAGAGACTTAAACACAGAGAAATTTTGTAGATTACCA 740
Db 537 GCACTCCCTCAACATCATTTTACAGGATCTGAAGCCAGAGAACATTTCTTTGACTGCCA 596
Qy 741 GGGACACATTTGCTTACTGACTTCGAGCTCTGCAAGAGGAGAACATTTGAACACACAGCAC 800
Db 597 GGGACACAGTGTGCTGACGAGATTTTGGCCTCTGCAAGGAAGGTGTAGAGCTTGAAGACAC 656
Qy 801 AACATCCACTTCTGTGGCAGCGCGAGTATCTCGCACCTGAGTGTCTTATAGAGAGCC 860
Db 657 CACATCCACATTTCTGTGGTACCCCTGAGTACTTTGGCACCTTGAAGTCTTCGGAAGAGCC 716
Qy 861 TTATGACAGAGCTGTGGAGTGTGGTGGAGCTGTCTTGTATGAGATGCTGTATGG 920
Db 717 TTATGATCGAGCAGTGGAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 776
Qy 921 CTTGCCGCCCTTTTATAGCCGAAACACAGCTGAAATGTACGACAACTTCTGAACAGGCC 980

Db 777 CCTGCCGCTTCTACAGCCAGATGTATCCAGATGTATGAGAAATCTGCACAGCC 836
 Qy 981 TCTCCAGTGAACCAATATTACAAATTCGCAAGACACTCTCTGGAGGCTCTCTGCA 1040
 Db 837 GCTACAGATCCCGAGCGCGAGTGGCGCTGTGACCTCTGCAAGCTCTCTCCA 896
 Qy 1041 GAAGCAGGACAAAGCGCTCGGGCAAGGATGACTTCTATGGAGATTAAGATCATGT 1100
 Db 897 CAAGGACGAGGCGCGCTGCGCTCCAAGCAGACTTTCTTGAGATTGAACCATGT 956
 Qy 1101 CTTCTCTCTTAATTAAGTGGATGATCTCATTAATAAGAGATTACTCCCTTTTAA 1160
 Db 957 ATTCTTCAGCCCAATACTGGATGACCTGTACCACAGAGGTAATCACTCACTCAA 1016
 Qy 1161 CCCAAATGTAGTGGGCGCAACGACCTACGCGACTTTGACCCCGAGTTTACCGAAGACC 1220
 Db 1017 CCCAAATGTACAGGACCTGCTGACTTGAAGCATTTTGACCCAGATTACCCAGGAGC 1076
 Qy 1221 TGTCCCACTCCATTGGCAAGTCCCTGACAGGCTCTGTACACGCCAGCGTCAAGGA 1280
 Db 1077 TGTGTCCAAGTCCATTGGCTGTACCCCTGACACTGT-----GGCCAGCAGCTCTGG 1127
 Qy 1281 AGTCCGAGGCTTTCTAGCTTTTCTATGCGCC 1316
 Db 1128 GGCCTCAAGTGCATTCTCGGATTTCTTATGCGCC 1163

RESULT 14

AAA27856
 ID AAA27856 standard; cDNA; 1834 BP.

XX AAA27856;

12-SEP-2000 (first entry)

Human serum and glucocorticoid-induced protein kinase 2-alpha cDNA.

Serum and glucocorticoid-induced protein kinase 2; SGK2-alpha;
 human; phosphorylation; cancer; diabetes; ischaemia; therapy; ss.

XX Homo sapiens.

Key Location/Qualifiers
 CDS 88..1191
 /*tag= a

XX WO200035946-A1.

XX 22-JUN-2000.

XX 14-DEC-1999; 99WO-GB04232.

XX 14-DEC-1998; 98US-0112217.

XX 19-AUG-1999; 99GB-0019676.

XX (UYDU-) UNIV DUNDEE.

XX Cohen P, Kobayashi T, Deak M;

XX WPI; 2000-442364/38.

XX P-PSDB; AAY95275.

Modulation of serum and glucocorticoid-induced protein kinase (SGK) by
 phosphorylation with 3-phosphoinositide-dependent protein kinase-1
 (PK1) or dephosphorylation, useful for treatment of cancer, diabetes
 and ischemic diseases -

XX Disclosure; Page 26-27; 127pp; English.

XX The present sequence is that of cDNA coding for human serum and
 glucocorticoid-induced protein kinase (SGK) isoform 2-alpha (see
 AAY95275). SGK (see AAY95279) was initially identified as a
 glucocorticoid and osmotic stress-responsive gene. Novel isoforms,

CC SGK2 and SGK3, were isolated from EST database searches, and 2
 CC splice variants of SGK2, i.e. SGK2-alpha and -beta (see AAY95276),
 CC which contains an extra 60 N-terminal residues, were identified.
 CC SGK2-alpha is expressed in liver, kidney, pancreas and brain. It
 CC is activated by phosphorylation in a similar manner to SGK. The
 CC invention provides methods of activating SGK activity by
 CC phosphorylation using 3-phosphoinositide-dependent protein kinase-1
 CC (PK1), and of reducing the activity of SGK by dephosphorylation.
 CC The invention also provides a method of identifying a compound that
 CC modulates the activity of SGK. Such compounds are useful for
 CC treating patients requiring modulation of SGK, such as patients
 CC with cancer, diabetes or ischaemic disease.

XX SQ Sequence 1834 BP; 483 A; 470 C; 470 G; 411 T; 0 other;

Query Match 39.4%; Score 527.2; DB 21; Length 1834;
 Best Local Similarity 69.5%; Pred. No. 4.1e-145;
 Matches 734; Conservative. 0; Mismatches 313; Indels 9; Gaps 1;

Qy 261 TTCTCTCCACCAAGTCCTTCTCAGCAATCAACCTTGGCCCTCGTCCAACTCTCATGC 320
 Db 117 TCCACAGCCCTCCAGGCGCAATGGGAACATCAACCTGGGCGCTTCAGCCAAACCAATGC 176
 Qy 321 TAAACCATCTGACTTTCACCTTTTGAAGTATCGGAAGGCGAGTTTGGAAAGGTCT 380
 Db 177 CCAGCCGACGGACTTCGACTTCTCAAGTCTATCGGAAGGGAACCTACCGGAAGGTCT 236
 Qy 381 TCTAGCAAGACACAAGCGCAGAGAGTGTCTATGTCAGTCAAGTCTTACAGAGAAAGC 440
 Db 237 ACTGGCCAAAGCGCAAGTGTATGGGCGTCTATGTCAGTCAAGTCTTACAGAAAGTC 296
 Qy 441 AATCTCTGAAAGAAAGAGAGAGCATATTTATGTCGGAGCGGAATGTTCTGTGAGAA 500
 Db 297 CATCTTAAAGAAAGAGAGAGCAGCCACATCATGGCAGGCGAGTGTCTTCTGAAGAA 356
 Qy 501 TGTGAAGACACCTTTCTCGTGGGCTTCACTTCTTCCAGACTGTGACAAATGTGA 560
 Db 357 CGTGGCGACCCCTTCTCGTGGGCTTCACTTCTTCCAGACACCTTGAAGGCTCTA 416
 Qy 561 CTTTGTCTAGACTACATTAATGTTGAGAGTGTCTTACCATCTCCAGGAGGACGCTG 620
 Db 417 CTTGTGTCTGACTATGTCAACGGGGGAGAGTCTTCTTCCACCTCAGCGGGAGCGCG 476
 Qy 621 CTTCTCTGAAACCAAGCGGCTCGTTTCTATGCTGCTGAAATAGCCAGTGCCTTGGCTACCT 680
 Db 477 GTTCTCTGGAGCCCGCGCCAGGTTCTACGCTGCTGAGTGGCCAGCGCATTTGGCTACCT 536
 Qy 681 GCATTCATCTGAACATCGTTTATAGAGACTTAAACCCAGAGAAATTTTGTAGATTCA 740
 Db 537 GCATCTCCCTCAACATCATTTACAGGGATCTGAAACCAGAGAACATTTCTTTGACTGCCA 596
 Qy 741 GGGACACATTTCTTACTGACTTCCGACTCTGCAAGGAGAACATTTGAACACACAGCAC 800
 Db 597 GGGACACGTTGCTGACGGATTTTGGCGCTCTGCAAGGAGGTTGAGAGCTTGAAGCAC 656
 Qy 801 AACATCCACTCTGTGGCAGCGCGAGTATCTCGCACCTCGAGGTGCTTCTATAGAGGCC 860
 Db 657 CACATCCACATTTCTGTGTACCCCTGAGTACTTTGGCACCTGAGTCTTCGGAAGAGCC 716
 Qy 861 TTATGACAGGACTGTGGACTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 920
 Db 717 TTATGATCAGCAGTGGACTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 776
 Qy 921 CCTGCGCGCTTTTATAGCGGAAACACAGCTGAATGTAGGACAACTTCTGAACAGGCC 980
 Db 777 CCTGCGCGCTTCTACAGCCAAAGATGTATCCCAGATGTATGAGAACATTTCTGACCCAGCC 836
 Qy 981 TCTCCAGCTGAAACCAATATTACAAATTCGCAAGACACCTCTCGAGGGCTCTCTGCA 1040
 Db 837 GCTACAGATCCCGGAGGCGGACAGTGGCGGCTGTGACCTCTCTGCAAGGCTTCTCCA 896
 Qy 1041 GAAGGACAGGACAAAGCGCTCGGGCCCAAGGATGACTTTCATGAGATTAAAGAGTCTGT 1100

Search completed: June 25, 2003, 08:31:27
Job time : 247 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 06:39:20 ; Search time 2375 Seconds
(without alignments)
16395.602 Million cell updates/sec

Title: US-10-067-977-1

Perfect score: 1338

Sequence: 1 atggggagatgcaggcg.....ccacggactttctctctga 1338

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.ty.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg_hum.*
31: em.htg_inv.*
32: em.htg_other.*
33: em.htg_mus.*
34: em.htg_pln.*
35: em.htg_rnd.*
36: em.htg_mam.*
37: em.htg_vrt.*
38: em.sy.*
39: em.htgo_hum.*
40: em.htgo_mus.*
41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1221.4	91.3	2364	9	AK098509	AK098509 Homo sapi
2	1221.4	91.3	2382	9	AF153609	AF153609 Homo sapi
3	1221.4	91.3	2382	9	BC001263	BC001263 Homo sapi
4	1219.8	91.2	2311	6	AR151390	AR151390 Sequence
5	1219.4	91.1	3196	9	AK055077	AK055077 Homo sapi
6	1218.2	91.0	1296	6	AX056374	AX056374 Sequence
7	1218.2	91.0	2370	6	AR179441	AR179441 Sequence
8	1218.2	91.0	2370	6	AX002570	AX002570 Sequence
9	1218.2	91.0	2370	6	AX337834	AX337834 Sequence
10	1218.2	91.0	2370	6	AX411211	AX411211 Sequence
11	1218.2	91.0	2370	9	HSRNAS1PK	Y10032 H. sapiens m
12	1144	85.5	2281	6	AX017284	AX017284 Sequence
13	1068.6	79.9	1920	4	AF139639	AF139639 Oryctolag
14	1015	75.9	2429	10	AF139638	AF139638 Mus muscu
15	1010.2	75.5	2426	10	AF205855	AF205855 Mus muscu
16	1008.6	75.4	2423	10	BC005720	BC005720 Mus muscu
17	983	73.5	2435	10	RATSGPK	L01624 Rattus norv
18	978.8	73.2	2432	6	AX056375	AX056375 Sequence
19	814.8	60.9	1417	5	AF057138	AF057138 Xenopus l
20	705	52.7	2470	5	SAC223715	AJ223715 Squalus a
21	705	52.7	3105	5	SAC223716	AJ223716 Squalus a
22	533.2	39.9	1803	10	AF312007	AF312007 Mus muscu
23	533.2	39.9	2494	10	BC018363	BC018363 Mus muscu
24	527.2	39.4	1812	6	AX056472	AX056472 Sequence
25	527.2	39.4	1812	6	AX399684	AX399684 Sequence
26	527.2	39.4	1812	9	AF169034	AF169034 Homo sapi
27	527.2	39.4	1815	9	BC014037	BC014037 Homo sapi
28	527.2	39.4	1834	6	AX026166	AX026166 Sequence
29	527.2	39.4	2146	6	AX026164	AX026164 Sequence
30	527.2	39.4	2146	9	AF186470	AF186470 Homo sapi
31	520.4	38.9	1768	9	BC015326	BC015326 Homo sapi
32	520.4	38.9	2391	9	AF169035	AF169035 Homo sapi
33	520.4	38.9	2404	6	AX026165	AX026165 Sequence
34	520.4	38.9	2512	6	E32369	E32369 Serine-thre
35	515.6	38.5	3984	9	AF085233	AF085233 Homo sapi
36	495.4	37.0	2476	10	AF169033	AF169033 Mus muscu
37	481	35.9	2184	10	BC026549	BC026549 Mus muscu
38	451.2	33.7	195843	2	AC103256	AC103256 Rattus no
39	448.6	33.5	906	10	AF361756	AF361756 Rattus no
40	437.2	32.7	1659	10	BC002222	BC002222 Mus muscu
41	407.6	30.5	21455	2	AC124486	AC124486 Mus muscu
42	356.2	26.6	1346	6	AX056376	AX056376 Sequence
43	292.8	21.9	1662	3	AB060291	AB060291 Asterina
44	283.8	21.2	2445	3	AY069856	AY069856 Drosophil
45	283.8	21.2	3647	3	DMDAKT1	Z26242 D.melanog

ALIGNMENTS

RESULT 1
AK098509

LOCUS
DEFINITION
AK098509
Homo sapiens CDNA FLJ25643 fis, clone STM07148, highly similar to
SERINE/THREONINE-PROTEIN KINASE SGK (EC 2.7.1.-).

ACCESSION
VERSION
KEYWORDS
SOURCE
AK098509
AK098509.1 GI:21758535
oligo capping; fis (full insert sequence).
Homo sapiens stomach mucosa cDNA to mRNA, clone lib:STM
clone:STM07148.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1
Ishibashi, T., Kanehori, K., Yosida, M., Watanabe, S., Ishida, S.,

Ono, Y., Hotuta, T., Hiraoka, S., Murakawa, K., Takiguchi, S.,
Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M.,
Yamashita, H., Chida, Y., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S.,
Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H.,
Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and
Sugano, S.

NEDO human cDNA sequencing project

Unpublished

2 (bases 1 to 2364)

Sugano, S. and Suzuki, Y.

Direct Submission

Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
E-mail: cdna@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286,
Fax: 81-3-5449-5416

NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB; clone selection for
full insert sequencing: RAB and Helix Research Institute.

Location/Qualifiers

1. .2364

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="STM07148"

/tissue_type="stomach mucosa"

/clone_lib="STM"

/notes="cloning vector: pME18SFL3"

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BASE COUNT
ORIGIN

Query Match 91.3%; Score 1221.4; DB 9; Length 2364;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	116	TGCGTTTCATGAGCAGCAGAGAGATGGTCTGAACGACTTTATTTCAGAAGATTGCCAATA	175
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QY	176	ACTCCTATGATGCAACACCCCTGAAGTTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG	235
DB	191	ACTCCTATGATGCAACACCCCTGAAGTTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG	250
QY	236	AGCCTGAGCTTATGAATGCCAACCCCTTCTCCTCCACCAAGTCTCTTCAGCAAAATCAACC	295
DB	251	AGCCTGAGCTTATGAATGCCAACCCCTTCTCCTCCACCAAGTCTCTTCAGCAAAATCAACC	310
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DB	311	TTGGCCGCTGCTGCAATCTCTGATGCTTAACCATCTGACTTTTCATCTTTGAAAAGTATCG	370
QY	356	GAAGGCGCAGTTTGGAAAGTTCTTCTAGCAGACACCAAGGAGGAGAGTGTCTTATG	415
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DB	431	CAGTCAAAAGTTTACAGAAGAAAGCAATCTGAAAAGAAAGAGGAGCAATATTATGT	490
QY	476	CGAGCGGAATGTCTGTGAAGATGTGAAGCACCCTTTCTGTTGGGCTTCACCTTCT	535
DB	491	CGAGCGGAATGTCTGTGAAGATGTGAAGCACCCTTTCTGTTGGGCTTCACCTTCT	550
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DB	551	CTTTCAGAGCTGCTGACAAATTGACTTTCTCTAGACTACATTAAATGGTGGAGAGTTGT	610
QY	596	TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACACCGGGCTCGTTCTATGCTGCTG	655
DB	611	TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACACCGGGCTCGTTCTATGCTGCTG	670

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DB	671	AAATAGCCAGTGCCTTGGGCTACCTGCATTCACTGAACATCGTTTATAGAGACTTAAAC	730
QY	716	CAGAGAATATTTTGTAGATTTCACAGGGACACATTGTCTTACTGACTTCGGACTCTGCA	775
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QY	776	AGGAGAACATTGAACAACAACAGACAAATCCACCTTCTGTGGCAGCGCGAGATATCTCG	835
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QY	836	CACCTGAGTGTCTTATAGCAGCCTTATGACAGGACTGTGAGTGGTGGTCTGGGAG	895
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QY	896	CTGTCTTGTATGAGATGCTGTATGGCTCGCGCTTTTATAGCCGAAACACACAGCTGAAA	955
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QY	956	TGTACGACAACTTCTGAACAAGCCTCTCCAGCTGAACCAATATATACAAATTCGCGAA	1015
DB	971	TGTACGACAACTTCTGAACAAGCCTCTCCAGCTGAACCAATATATACAAATTCGCGAA	1030
QY	1016	GACACCTCTGGAGGCGCTCTCCAGAGCAGGACAAAGCGCTCGGGGCCAAGATG	1075
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QY	1076	ACTTCATGGAGATTAAAGATGATGTCTTCTCTCTTAATTAACCTGGGATGATCTCATTA	1135
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QY	1196	TTGACCCCGAGTTTACCGAAGAGCCTGTCCTCCCACTCCATTGGCAAGTCCCTTGACAGCG	1255
DB	1211	TTGACCCCGAGTTTACCGAAGAGCCTGTCCTCCCACTCCATTGGCAAGTCCCTTGACAGCG	1270
QY	1256	TCTCTGTACAGCCAGCGTCAAGGAGCTGCCAGGCTTTCTTAGGCTTTTCTATGCGC	1315
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QY	1316	CTCCACGAGCTTTTCTCTCTGA	1338
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RESULT 2

AF153609

LOCUS

DEFINITION

ACCESION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

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TITLE

JOURNAL

AF153609 2382 bp mRNA linear PRI 28-JUN-1999
Homo sapiens serine/threonine protein kinase sgk mRNA, complete cds.

AF153609

AF153609.1 GI:5231142

Homo sapiens.

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2382)

Kim, M.K., Kim, Y.H., Seo, J.M., Lee, H.M., Chung, H.J., Sohn, M.Y.,

Hwang, S.Y., Im, S.U., Jung, E.J. and Kim, J.C.

A catalogue of genes in the human dermal papilla cells as

identified by expressed sequence tags

Unpublished

2 (bases 1 to 2382)

Kim, M.K., Kim, Y.H., Suh, J.M., Lee, H.M., Chung, H.J., Sohn, M.Y.,

Hwang, S.Y., Im, S.U., Jung, E.J. and Kim, J.C.

Direct Submission

Submitted (24-MAY-1999) Immunology, Kyungpook National University,

School of Medicine, 101 Dongin Dong, Jung Gu, Taegu, Taegu 700-422,
South Korea

FEATURES

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BASE COUNT 640 a 519 c 513 g 710 t
ORIGIN

Query Match 91.3%; Score 1221.4; DB 9; Length 2382;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	116	TGCGTTTCATGAACGAGGAGGATGGCTGACGACTTATTCAGAGATTCGCCAATA	175
DB	116	TCGCTTTCATGAACGAGGAGGATGGCTGACGACTTATTCAGAGATTCGCCAATA	175
QY	176	ACTCCTATGATGCAACACCTGAACTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG	235
DB	176	ACTCCTATGATGCAACACCTGAACTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG	235
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DB	236	AGCTGAGCTTATGAATGCAACCCCTTCTCTCCACCAAGTCTTTCAGCAAAATCAACC	295
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DB	296	TTGGCCCGTCCATCTCATGCTAAACCATCTGACTTTCACCTTCTTGAAGTATCG	355
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DB	476	CGAGCGGAGTGTCTGTTCAAGATGTGAAGACCCCTTCTGTTGGGCTTCACCTTCT	535
QY	536	CTTTCACAGCTGCTGACAAATGTACTTCTCTAGACTACATTAATAGTGGAGAGTTGT	595
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QY	596	TCTACCATCTCCAGAGGAAACGCTGCTTCTGGAACCAACGCGGCTCGTTTCTATGCTGCTG	655
DB	596	TCTACCATCTCCAGAGGAAACGCTGCTTCTGGAACCAACGCGGCTCGTTTCTATGCTGCTG	655
QY	656	AAATAGCAGTGCCTGGGCTACTGCAATTCAGTGAACATCGTTTATAGAGACTTAAAC	715
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DB	836	CACCTGAGTGTCTTATGAAGAGCCTTATGACAGGACTGTGACTGCTGTGCTCTGGAG	895
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QY	956	TGTACGACAAACATTCTGAACAGCCTTCTCAGCTGAAACCAATATATACAAATTCGCAA	1015
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RESULT 3
BC001263
LOCUS

DEFINITION Homo sapiens, serum/glucocorticoid regulated kinase, clone MGC:5030
IMAGE:3459056, mRNA, complete cds.
ACCESSION BC001263
VERSION BC001263.1 GI:12654838
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2382)
AUTHORS Strausberg R.
TITLE Direct Submission
JOURNAL Submitted (11-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 4 Row: a Column: 12
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 5032090.

FEATURES

Location/Qualifiers
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 /clone_lib="NIH_MGC_12"
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 /note="Vector: pCMV-SPORT6"
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CDS

BASE COUNT 642 a 519 c 513 g 708 t
 ORIGIN
 Query Match 91.3%; Score 1221.4; DB 9; Length 2382;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	116	TGGCTTTTCATGACGACGAGGAGTGGTCTGAACGATTTTATTCAGAGATTGCCAATA	175
Db	116	TCGCTTTTCATGACGACGAGGAGTGGTCTGAACGATTTTATTCAGAGATTGCCAATA	175
Qy	176	ACTCCTATGATGACACACCCCTGAGTTCAGTCCATCTTGAAGATCTCCCACTCAGG	235
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Qy	656	AAATAGCCAGTGGCTTGGGCTACTGCAATTCATGCAATCTGTAAGACTTAAAC	715
Db	656	AAATAGCCAGTGGCTTGGGCTACTGCAATTCATGCAATCTGTAAGACTTAAAC	715

Qy	716	CAGAGAATATTTTGTAGATTTCACAGGACACATTTCTTACTTACTGACTTCGGACTCTGCA	775
Db	716	CAGAGAATATTTTGTAGATTTCACAGGACACATTTCTTACTTACTGACTTCGGACTCTGCA	775
Qy	776	AGGAGAACATTTGAACACACAGCACCAATCCACCTTTCTGTGGCAGCGCGAGTATCTCG	835
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Db	836	CACCTGAGGTCTTCAAGCAGCCTTATGACAGGACTGTGGAGCTGGTGGTCTGGGAG	895
Qy	896	CTGTCTTGTATGAGATGCTGTATGGCTCGCGCTTTTATAGCCCAACACAGCTGAAA	955
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Qy	1016	GACACCTCTCGAGGCGCTCTGCGAGAGGACAGGACAAAGCGGCTCGGGGCGCAAGATG	1075
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Qy	1076	ACTTCATGAGATTAAAGAGTCATGCTCTTCTCTTAAATTAACCTGGGATGATCTCATTA	1135
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Qy	1256	TCTCTGTACAGCGGCTCAAGGAGCTGCGGAGCTTTCTTAGGCTTTTCTTATGCGC	1315
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RESULT 4
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 DEFINITION Sequence 6 from patent US 6232077.
 ACCESSION AR151390
 VERSION AR151390.1 GI:15117440
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 2311)
 AUTHORS Au-Young, J., Guegler, K.J. and Hawkins, P.R.
 TITLE Human protein kinases
 JOURNAL Patent: US 6232077-A 6 15-MAY-2001;
 FEATURES Location/Qualifiers
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 BASE COUNT 604 a 508 c 506 g 692 t 1 others
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Query Match 91.2%; Score 1219.8; DB 6; Length 2311;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	116	TGGCTTTTCATGACGACGAGGAGTGGGCTGCAACGATTTTATTCAGAGATTGCCAATA	175
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ACCESSION
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AUTHORS
Nishi, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A.,
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and Isogai, T.
NEDO human cDNA sequencing project
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 3196)
AUTHORS
Isogai, T., Otsuki, T. and Sugiyama, T.
DIRECT SUBMISSION
JOURNAL
COMMENT
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
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Evaluation; clone selection for full insert sequencing: RAB and
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 REFERENCE 1 (bases 1 to 1296)
 AUTHORS Plozman, G.D., Martinez, R., Whyte, D. and Sudersanam, S.
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VERSION AX002570.1 GI:7242111
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 2370)
JOURNAL Lang.F.P. and Waldegger, S.D.
DADE BEHRING MARBURG GMBH (DE)
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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JOURNAL Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
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REFERENCE 1
AUTHORS Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 3858 11-APR-2002;
GENE LOGIC INC (US)
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DEFINITION Sequence 39 from Patent WO947669.
ACCESSION AX017284
VERSION 1 (bases 1 to 2281)
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 2281)
AUTHORS Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
Pilarczyk,C.
TITLE Human nucleic acid sequences from tissue of breast tumors
JOURNAL Patent: WO 947669-A 39 23-SEP-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
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 kinase (Sgk) mRNA, complete cds.
 ACCESSION AFI39639
 VERSION AFI39639.1 GI:5442270
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 REFERENCE 1 (bases 1 to 1920)
 Naray-Fejes-Toth, A., Canessa, C., Cleaveland, E. S., Aldrich, G. and
 Fejes-Toth, G.
 TITLE sgk is an aldosterone-induced kinase in the renal collecting duct.
 Effects on epithelial Na⁺ channels
 J. Biol. Chem. 274 (24), 16973-16978 (1999)
 JOURNAL 99287894
 MEDLINE 10358046
 PUBMED 2 (bases 1 to 1920)
 Naray-Fejes-Toth, A. and Fejes-Toth, G.
 REFERENCE Direct Submission
 AUTHORS Naray-Fejes-Toth, A. and Fejes-Toth, G.
 TITLE Submitted (31-MAR-1999) Physiology, Dartmouth Medical School, 1
 JOURNAL Medical Center Drive, Lebanon, NH 03756, USA
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DEFINITION      (Sgk) mRNA, complete cds.
ACCESSION      AF139638
VERSION      AF139638.1
KEYWORDS      GI:5442268
SOURCE      Mus musculus.
ORGANISM      Mus musculus
REFERENCE      1 (bases 1 to 2429)
AUTHORS      Naray-Fejes-Toth,A., Canessa,C., Cleaveland,E.S., Aldrich,G. and
      Fejes-Toth,G.
TITLE      Sgk is an aldosterone-induced kinase in the renal collecting duct.
MEDLINE      Effects on epithelial na+ channels
J. Biol. Chem. 274 (24), 16973-16978 (1999)
PUBMED      99287894
REFERENCE      2 (bases 1 to 2429)
AUTHORS      Naray-Fejes-Toth,A. and Fejes-Toth,G.
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JOURNAL      Submitted (31-MAR-1999) Physiology, Dartmouth Medical School, 1
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LOCUS      Mus musculus serum and glucocorticoid-dependent protein kinase
DEFINITION      (Sgk) mRNA, complete cds.

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 Shigaev.A., Asher.C., Latter.H., Garty.H. and Reuveny.E.
 Regulation of sgk by aldosterone and its effects on the epithelial
 Na(+) channel
 Am. J. Physiol. Renal Physiol. 278 (4), F613-F619 (2000)
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 2 (bases 1 to 2426)
 Shigaev.A., Asher.C., Latter.H., Garty.H. and Reuveny.E.
 Direct Submission
 Submitted (17-NOV-1999) Biological Chemistry, Weizmann Institute,
 Rehovot 76100, Israel
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 QY 236 AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTCTTCAGCAAAATCAACC 295
 DB 259 AGCCGAGCTTATGAACGCTAAACCCCTCTCTCCGCGCAAGTCCCTCTCAACAAATCAACC 318
 QY 296 TTGGCCCGTCTGCTCAATCTCATGCTAAACATCTGACTTTTCATCTTCTGAAAGTATCG 355
 DB 319 TGGGTCCGTCTCTCAACCCCTCAGCCAAACCCCTCCGACTTCTTCTTCTGAAAGTATCG 378
 QY 356 GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAGACACAGGCGAGAGAAAGTGTCTATG 415
 DB 379 GAAAGGCGAGTTTGGAAAGGTTCTTCTGCTAGGACACAGGCGAGAGAAAGTATCTATG 438
 QY 416 CAGTCAAAGTTTACAGAGAAAGCAATCTGTAAGAAAGAAAGAGGAGAGCAATATTATGT 475
 DB 439 CAGTCAAAGTTTACAGAGAAAGCAATCTGTAAGAAAGAAAGAGGAGAGCAATATTATGT 498

Search completed: June 25, 2003, 09:16:41
 Job time : 2386 secs

QY 476 CGGAGCGGAATGTTCTGTTGAAGAAATGTGAAGCACCCCTTTCTGTGGTGGCCCTCACTTCT 535
 DB 499 CAGAGCGGAATGTTCTGTTGAAGAAATGTGAAGCACCCCTTTCTGTGGTGGCCCTCACTTCT 558
 QY 536 CTTTCCAGACTCTGACAAATTTGTACTTTGTCTAGACTACATTAATATGTGGAGAGTTGT 595
 DB 559 CATTCCAGACCGCTGACAGCTCTACTTTGTCTGAGCTACATTAATATGTGGAGAGCTGT 618
 QY 596 TCTACCATCTCCAGAGGAGAGCTGCTCTCTGGAACACGGGCTCGTTTCTATGCTGCTG 655
 DB 619 TCTACCATCTCCAGAGGAGAGCTGCTCTCTGGAACACGGGCTCGATTCTACGAGCTG 678
 QY 656 AATAGCCAGTGCCTTTGGGCTACCTGCAATCTCACTGAACATCGTTTATAGAGACTTAAAC 715
 DB 679 AATAGCCAGTGCCTTTGGGCTATCTGCACTCCCTAAACATCGTTTATAGAGACTTAAAC 738
 QY 716 CAGAGAAATATTTGTCTAGATTTCACAGGAGACATTTGTCTTACTGACTTCGGAAGCTGCA 775
 DB 739 CTGAGAAATATTTCTCTAGACTCCAGGGGACATCGTCTCTACTGACTTTGGGCTCTGCA 798
 QY 776 AGAGAAATATTTGAACACACAGACACAAATCCACCTTCTGTGGCACGCCGGAGTATCTCG 835
 DB 799 AAGAGAAATATTTGAGCATAAACGGGACAAATCTACCTTCTGTGGCACGCCGTAGTATCTCG 858
 QY 836 CACCTGAGTGTCTTCAATAGCAGCCTTATGACAGGACTGTGAGCTGCTGCTGCTGGAG 895
 DB 859 CTCTGAGTGTCTTCCATAGCAGCCTTATGACAGGAGCTGAGCTGCTGCTGCTGGG 918
 QY 896 CTGCTTGTATGAGATGCTGTATGGCTGCTGCCCTCTTTTATAGCCGAAACACAGCTGAAA 955
 DB 919 CTGCTGATGATGAGTGTCTACGGCTGCTGCCCTCTTTTATAGCCGAAACACGGCTGAGA 978
 QY 956 TGTAGCAACATTTCTGAACAGCCTCTCCAGCTGAACCAATATTTACAAATTCGCGAA 1015
 DB 979 TGTAGCAACATTTCTGAACAGCCTCTCCAGTGAACCAATATTTACAAATTCGCGAA 1038
 QY 1016 GACACCTCTGGAGGCTCTCTGACAGGACAGGACAAAGCGCTCGGGCCCAAGATG 1075
 DB 1039 GGACCTCTCTGGAAGCTCTCTGACAGGACAGGACAAAGCGCTGGGTGCCAAGATG 1098
 QY 1076 ACTTCATGGAGATTAAGAGTCAATGCTCTCTCTCTTAAATTAACCTGGGATGATCTCATTA 1135
 DB 1099 ACTTCATGGAGATTAAGAGTCAATATTTCTCTCTTAAATTAACCTGGGATGATCTCATCA 1158
 QY 1136 ATAAGAAGATTAATCTCCCTTTTAAACCAATGAGTGGGCCCCAACGACCTACGGCACT 1195
 DB 1159 ATAAGAAGATTAATCAACCCCAATTTAAACCAATGAGTGGGCCCCAGTGACCTTCGGCACT 1218
 QY 1196 TTGACCCCGAGTTTACCGAAGAGCCTGCTCCCAACTCCATTTGGCAAGTCCCTTGACAGCG 1255
 DB 1219 TCGATCCGAGTTTACCGAAGAGCCTGCTCCCAAGCTCCATTCGCGAGCTCCCTTGACAGCA 1278
 QY 1256 TCTCTGTCAGCCAGCGCTCAAGGAAGCTGCCAGAGCTTTCTTAGGCTTTTCTATGCGC 1315
 DB 1279 TCTCTGTCAGCCAGCGCTGAGGAAGAGCAGAGAGAGCTTTCTCTGCGCTTCTCTATGAC 1338
 QY 1316 CTCCCAAGGACTTTTCTCTGTA 1338
 DB 1339 CTCCTGTGATTTCTTCTCTGTA 1361

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:20:30 ; Search time 82 Seconds
(without alignments)
1118.183 Million cell updates/sec

Title: US-10-067-977-2

Perfect score: 2340

Sequence: 1 MGEVQALARLESLLRPR.....KEAAEFLGFSAPPTDSDL 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mnc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1984.5	84.8	434	13	O93524 xenopus lae
2	1825.5	78.0	594	13	O73927 squalus aca
3	1816	77.6	433	13	O73926 squalus aca
4	1484	63.4	429	11	O8VBK1 mus musculus
5	1484	63.4	496	11	O9ERE3 mus musculus
6	1476	63.1	496	4	O96BR1 mus musculus
7	1463	62.5	496	4	O9PL07 mus musculus
8	1419	60.6	427	4	O9HBY8 mus musculus
9	1411	60.3	367	11	O9UKG6 mus musculus
10	1387	59.3	367	11	O9QZS5 mus musculus
11	1374.5	58.7	366	11	O8RQ26 mus musculus
12	1236	52.8	302	11	O8R4U9 mus musculus
13	1082	46.2	422	5	O94365 caenorhabdi
14	951	40.6	185	11	O99LU4 mus musculus
15	912	39.0	465	4	O96QV3 mus musculus
16	909.5	38.9	486	5	O95YJ0 asterina pe

17	894	38.2	530	5	O24293 drosophila
18	894	38.2	530	5	O8T9A5 drosophila
19	894	38.2	611	5	O24469 drosophila
20	878	37.5	480	13	O57513 gallus gall
21	876.5	37.5	479	13	O8UUX0 brachydanio
22	872.5	37.3	481	13	O98TY9 xenopus lae
23	861	36.8	480	4	O9BWB6 homo sapien
24	843	36.0	640	3	O96VR1 tryphonectr
25	840	35.9	662	3	O99012 schizosacch
26	828	35.4	569	3	O9P7J8 trichoderma
27	814	34.8	546	5	O17942 caenorhabdi
28	811.5	34.7	482	4	O9BR80 caenorhabdi
29	811	34.7	501	13	O9W6Y9 xenopus lae
30	801.5	34.3	541	5	O17941 caenorhabdi
31	797	34.1	917	3	O9HGS0 botrytis ci
32	793.5	33.9	522	5	O9BMX7 aplysia cal
33	791.5	33.8	670	5	O9V7V6 drosophila
34	791.5	33.8	679	5	O9V7V7 drosophila
35	790	33.8	484	5	O9GQB3 artemia san
36	789	33.7	554	5	O95T78 drosophila
37	784	33.5	490	5	O94533 drosophila
38	784	33.5	637	5	P91656 drosophila
39	784	33.5	707	5	O20953 caenorhabdi
40	776.5	33.2	680	5	P90380 caenorhabdi
41	771	32.9	528	5	O9XTG7 caenorhabdi
42	770	32.9	673	5	O62567 suberites d
43	769	32.9	580	13	O90XF2 brachydanio
44	768.5	32.8	670	5	O01715 hydra atten
45	768.5	32.8	674	5	O01716 hydra atten

ALIGNMENTS

RESULT 1

O93524 ID O93524 PRELIMINARY; PRT; 434 AA.
AC O93524;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 49.1 kDa protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RENAL TUBULE;
RX MEDLINE=99162637; PubMed=10051674;
RA Chen S.Y., Bhargava A., Mastroberardino L., Meijer O.C., Wang J.,
RA Buse P., Firestone G.L., Verrey F., Pearce D.;
RA "Epithelial sodium channel regulated by aldosterone-induced protein
sgk.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:2514-2519(1999).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF057138; AAC62398.1; -;
DR HSSP; P00517; IYDR.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; I.
DR Pfam; PF00433; pkinase C; I.
DR ProDom; PD000001; Euk_pkinase; I.
DR SMART; SM00220; S_TKc; I.
DR SMART; SM00133; S_TK X; I.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 434 AA; 49130 MW; 4A061E38B6AA6F61 CRC64;


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Db 26 AFMKQKRWGLNDLQKLAASQSYACKHSSEVPAMLHIS-PAETEMNGTGASPPSPPTAQ 84
Qy 97 INLGPSSNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKEEKH 156
Db 85 INLGPSSNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKEEKH 144
Qy 157 IMSEKRVLLKXVHPFLVGLHFSFQADKLYFVLVDYINGGELFYHLQRECFLEPRARFY 216
Db 145 IMSEKRVLLKXVHPFLVGLHFSFQADKLYFVLVDYINGGELFYHLQRECFLEPRARFY 204
Qy 217 AAEATASALGYLHSLNIVYRDLKPNILDSQGHVLTDFGLCKENIEHNSTTSCFCTPE 276
Db 205 AAEATASALGYLHSLNIVYRDLKPNILDSQGHVLTDFGLCKENIEHNSTTSCFCTPE 264
Qy 277 YLAPEVLHKKQPYDRTVDWMCGLGAVLYEMLYGLPPFYSRNTAEMVDNLNKPQLKPNITN 336
Db 265 YLAPEVLHKKQPYDRTVDWMCGLGAVLYEMLYGLPPFYSRNTAEMVDNLNKPQLKPNISN 324
Qy 337 SARHLLGLLQKORTKRLGAKDDFMETKSHVFFSLINWDDLINKKITPPFPNPNVSGNDL 396
Db 325 SARHLLGLLQKORTKRLGAKDDFMETKSHVFFSLINWDDLINNAKLTTPFPNPNVSGPADL 384
Qy 397 RHPDPEETEERVPNSIGKSPDSVLVATSVKAEAEAFGLGFSYAPPTDSFL 445
Db 385 QHPDPEETEERVPNSIGKSPDSVLVATSVKAEAEAFGLGFSYAPPTDSFL 433

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RESULT 4

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Q8VEK1 ID Q8VEK1 PRELIMINARY; PRT; 429 AA.
AC Q8VEK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to serum/glucocorticoid regulated kinase-like.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018363; AAH18363.1; -
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR001683; PX.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR Pfam; PF00787; PX; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW Kinase.
SQ SEQUENCE 429 AA; 49077 MW; A9C6B7A0C34031F3 CRC64;

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Query Match 63.4%; Score 1484; DB 11; Length 429;
 Best Local Similarity 68.2%; Pred. No. 2.6e-114;
 Matches 281; Conservative 53; Mismatches 70; Indels 8; Gaps 3;

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Qy 41 FMKQKRWGLNDLQKLAASQSYACKHSSEVPAMLHIS-PAETEMNGTGASPPSPPTAQ 84
Db 19 FIKQKRWGLNDLQKLAASQSYACKHSSEVPAMLHIS-PAETEMNGTGASPPSPPTAQ 77
Qy 95 QQINLGPSSNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKEEKH 154

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Db 78 RNINLGPSSNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKEEKH 137
Qy 155 KHMISERNVLLKXVHPFLVGLHFSFQADKLYFVLVDYINGGELFYHLQRECFLEPRAR 214
Db 138 KHMISERNVLLKXVHPFLVGLHFSFQADKLYFVLVDYINGGELFYHLQRECFLEPRAR 197
Qy 215 FYAETASALGYLHSLNIVYRDLKPNILDSQGHVLTDFGLCKENIEHNSTTSCFCTPE 274
Db 198 FYAETASALGYLHSLNIVYRDLKPNILDSQGHVLTDFGLCKENIEHNSTTSCFCTPE 257
Qy 275 PEVLAPVLHKKQPYDRTVDWMCGLGAVLYEMLYGLPPFYSRNTAEMVDNLNKPQLKPNISN 334
Db 258 PEVLAPVLHKKQPYDRTVDWMCGLGAVLYEMLYGLPPFYSRNTAEMVDNLNKPQLKPNISN 317
Qy 335 TNSARHLLGLLQKORTKRLGAKDDFMETKSHVFFSLINWDDLINKKITPPFPNPNVSGNDL 394
Db 318 SLTAWMSILGLLQKORTKRLGAKDDFMETKSHVFFSLINWDDLINKKITPPFPNPNVSGNDL 377
Qy 395 DLHFPDPEETEERVPNSIGKSPDSVLVATSVKAEAEAFGLGFSYAPPTDSFL 445
Db 378 DLFDPDPEETEERVPNSIGKSPDSVLVATSVKAEAEAFGLGFSYAPPTDSFL 429

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RESULT 5

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Q9ERE3 ID Q9ERE3 PRELIMINARY; PRT; 496 AA.
AC Q9ERE3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Serine/threonine protein kinase CISK.
GN CISK.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20504817; PubMed=11050396;
RA Liu D., Yang X., Songyang Z.;
RT "Identification of CISK, a new member of the SGK kinase family that
RL Curr. Biol. 10:1233-1236(2000).
DR EMBL; AF312007; AAG34115.1; -
DR HSP; P05132; 1ATP.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR001683; PX.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR Pfam; PF00787; PX; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00312; PX; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 496 AA; 57145 MW; 4B7D2804A5948BAD CRC64;

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Query Match 63.4%; Score 1484; DB 11; Length 496;
 Best Local Similarity 68.2%; Pred. No. 3.2e-114;
 Matches 281; Conservative 53; Mismatches 70; Indels 8; Gaps 3;

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Qy 41 FMKQKRWGLNDLQKLAASQSYACKHSSEVPAMLHIS-PAETEMNGTGASPPSPPTAQ 84
Db 86 FIKQKRWGLNDLQKLAASQSYACKHSSEVPAMLHIS-PAETEMNGTGASPPSPPTAQ 144
Qy 95 QQINLGPSSNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKEEKH 154

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Db 145 RNINLPGTGNPHAKPTDFELKVGSGFKGLAKRKLKGKGYAVKVLQKTVLNARKEQ 204
Qy 155 KHMSENVLKKNVHPFLVGLHFSFOTADKLYFVLDYINGGELFVHLQRCFCLEPRAR 214
Db 205 KHMSENVLKKNVHPFLVGLHFSFOTADKLYFVLDYINGGELFVHLQRCFCLEPRAR 264
Qy 215 FYAAEIASALGYLHSLNIVYRDLPENILDSOGHIVLTDGFLCKENIEHNSTTSTFCGT 274
Db 265 FYAAEIASALGYLHSLNIVYRDLPENILDSOGHIVLTDGFLCKENIEHNSTTSTFCGT 324
Qy 275 PEYLAPEVLHKKQPYDRTVDMWCLGAVLYEMLYGLPPYPSYNTAEYDNLNKLQKLPNI 334
Db 325 PEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPYPSYNTAEYDNLNKLQKLPNI 384
Qy 335 TNSARHLLLEGLOKDKRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFPNVS 394
Db 385 SLTASLSLELLEKQNRNLGAKEDFLEIQNHFFESLSWTLVQKKIPPPFPNVS 444
Qy 395 DLRFHDFEETPEEPVNSIGKSPDVLVTASVKEAAEAFGLFSYAPPT-DSFL 445
Db 445 DIRNFDAVTEETVPYSCVSSDYSIVNASVLEADDAFVGFSAAPSEDLEL 496

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RESULT 6

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ID Q96BR1 PRELIMINARY; PRT; 496 AA.
AC Q96BR1; Q9UGS;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 57.1 kDa protein (Protein kinase).
GN SGK3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1.
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Strauberg R.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN 2.
RP SEQUENCE OF 68-496 FROM N.A.
RX MEDLINE=20018032; PubMed=10548550;
RT Kobayashi T., Deak M., Morrice N., Cohen P.;
RT "Characterization of the structure and regulation of two novel
RT isoforms of serum- and glucocorticoid-induced protein kinase.";
RL Biochem. J. 344:189-197(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; BC015326; A015326.1; -.
DR EMBL; AF169035; AAF12758.1; -.
DR HSP; P05132; IATP.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR001683; PX.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR Pfam; PF00787; PX; 1.
DR ProDom; PD000001; Euk_pkinase; 1..
DR SMART; SM00133; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN_1.
KW Hypothetical protein; ATP-binding; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 496 AA; 57108 MW; 76A6CCEB9006C1 CRC64;

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Query Match 63.1%; Score 1476; DB 4; Length 496;
 Best Local Similarity 67.5%; Pred. No. 1.5e-113;
 Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;

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Qy 41 FMKQRMGLNDFQKIANNYSACKHPEVOSILKIQOPELMNANPSPPP----- 91
Db 86 FIKQRMGLNDFQKIANNYSACKHPEVOSILKIQOPELMNANPSPPP----- 141
Qy 92 SPSQINLGPSGNPHAKPTDFELKVGSGFKGLAKRKLKGKGYAVKVLQKTVLNAR 151
Db 142 STSQINLGPSGNPHAKPTDFELKVGSGFKGLAKRKLKGKGYAVKVLQKTVLNAR 201
Qy 152 KEEKHIMSENVLKKNVHPFLVGLHFSFOTADKLYFVLDYINGGELFVHLQRCFCLEP 211
Db 202 KEQKHIMSENVLKKNVHPFLVGLHFSFOTADKLYFVLDYINGGELFVHLQRCFCLEP 261
Qy 212 RARFYAAEIASALGYLHSLNIVYRDLPENILDSOGHIVLTDGFLCKENIEHNSTTSTF 271
Db 262 RARFYAAEIASALGYLHSLNIVYRDLPENILDSOGHIVLTDGFLCKENIEHNSTTSTF 321
Qy 272 CGTPEYLAPEVLHKKQPYDRTVDMWCLGAVLYEMLYGLPPYPSYNTAEYDNLNKLQK 331
Db 322 CGTPEYLAPEVLHKKQPYDRTVDMWCLGAVLYEMLYGLPPYPSYNTAEYDNLNKLQK 381
Qy 332 PNITNSARHLLLEGLOKDKRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFPNVS 391
Db 382 PGVSLTASLSLELLEKQNRNLGAKEDFLEIQNHFFESLSWTLVQKKIPPPFPNVS 441
Qy 392 GPNDLRFHDFEETPEEPVNSIGKSPDVLVTASVKEAAEAFGLFSYAPPT-DSFL 445
Db 442 GPNDLRFHDFEETPEEPVNSIGKSPDVLVTASVKEAAEAFGLFSYAPPT-DSFL 496

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RESULT 7

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ID Q9P1Q7 PRELIMINARY; PRT; 496 AA.
AC Q9P1Q7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE SGK-like protein SGK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1.
RP SEQUENCE FROM N.A.
RX MEDLINE=20054360; PubMed=10585774;
RT Dai F., Yu L., He H., Zhao Y., Yang J., Zhang X., Zhao S.;
RT "Cloning and mapping of a novel human Serum/Glucocorticoid regulated
RT kinase-like gene, SGK, to chromosome 8q12.3-q13.1.";
RL Genomics 62:95-97(1999).
[2]
RN 2.
RP SEQUENCE FROM N.A.
RA Zhao Y.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF085233; AAF27051.2; -.
DR HSP; P05132; IATP.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR001683; PX.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR Pfam; PF00787; PX; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00132; PX; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
SQ SEQUENCE 496 AA; 56995 MW; DAAE2E736C90822C CRC64;

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Query Match 62.5%; Score 1463; DB 4; Length 496;
 Best Local Similarity 67.0%; Pred. No. 1.8e-112;
 Matches 278; Conservative 51; Mismatches 72; Indels 14; Gaps 3;

QY 41 FMKRRMGLNDFIKIANNVYACKHPEVQSILKISQPOPELMNANSPPP-----91
 DB 86 FIKRRAGLNEFIQNLVRYPELYNHPDVRAFLQWDSFKH-----QSGSEDEDESSQKLH 141
 QY 92 SPSQINLGPSNPHAKSPDFHFKVIGKSGFGKVLARHKAEEVFYAVKVLQKAILKK 151
 DB 142 STSQINILGPGNPHAKSPDFDFLKVIGKSGFGKVLAKRDLGKVAVKVLQKIVLNR 201
 QY 152 KEEKHIMSERVNLKVKHPELVGLHFSFQADKLYFLVDLYNGGELFYHLORERCLEP 211
 DB 202 KEQKHIMAEARNVNLKVKHPELVGLHYSFQTEKLYFLVDLYNGGELFFHLQERSPEH 261
 QY 212 RARYFAAEIASALGYLSNIVYDLKPENILDSQGHIVLTDGLCKENIEHNSSTSTF 271
 DB 262 RARYFAAEIASALGYLSIKIVYDLKPENILVDSVGHVLTDFGLCKEIAISDTITTF 321
 QY 272 CGTEYLAPEVLHKOPYDRYVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKLQK 331
 DB 322 CGTEYLAPEVIRKOPYDNTVDMWCLGAVLYEMLYGLPPFYCRVDAEYDNLNKLPLSLR 381
 QY 332 PNITNSARHLEGLLQKDRTELCAKODFMEIKSHVFFSLINWDDLKNTTPPNPNVS 391
 DB 382 PGVSLRAWSILEELEXKDRQLKAKEDFLEIQNHPPFESLSWADLVQKKTTPPNPNVA 441
 QY 392 GPNDLRHFDPEETPEEPNPSIGKSPDSVLVTASVKEAAEAFGLFSYAPPT-DSFL 445
 DB 442 GPDIRNFDTAETETVPYSCVSDYSIVNASVLEADDAFVGFSYAPPSSEDLFL 496

RESULT 8

Q9HBY8 PRELIMINARY; PRT; 427 AA.
 AC Q9HBY8
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Protein kinase.
 GN SGK2BETA
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20018032; PubMed=10548550;
 RA Kobayashi T., Deak M., Morrice N., Cohen P.;
 RT "Characterization of the structure and regulation of two novel
 RT isoforms of serum- and glucocorticoid-induced protein kinase.";
 RL Biochem. J. 344:189-197(1999).
 DR EMBL; AF186470; AAG17012.1; -.
 DR HSSP; P05132; IATP.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase C; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00133; S_TKc; 1.
 DR SMART; SM00219; TYRKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Transferase
 SQ SEQUENCE 427 AA; 47604 MW; D8F0FA6DF54B1370 CRC64;

Query Match

60.6%; Score 1419; DB 4; Length 427;

Best Local Similarity 68.3%; Pred. No. 6.2e-109;
 Matches 267; Conservative 56; Mismatches 54; Indels 14; Gaps 4;

QY 66 PEVQSIKIKSQPOPEL-----MNANP---SPPPSPSQ---QINLGPSNPHAKSPDFH 114
 DB 38 PPTPTLSCLLLPVPPELPDHCYRMNSSPAGTSPQPSRANGNINLGFSANPNAOPTDFDP 97
 QY 115 LKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIMSERVNLKVKHPELV 174
 DB 98 LKVIKGNVGVLLAKRKSDFYAVKVLQKLSILKKKEQSHIMAEARSVLLKNVRHPELV 157
 QY 175 GLHFSFQADKLYFLVDLYNGGELFYHLORERCLEPRARFYAAEIASALGYLSNIVY 234
 DB 158 GLRYSFQTEKLYFLVDLYNGGELFFHLQERRRFLPRARFYAAEIASALGYLSNIIY 217
 QY 235 RDLKPENILDSQGHIVLTDGLCKENIEHNSSTSTFCGTEYLAPEVLHKOPYDRYVDM 294
 DB 218 RDLKPENILDSQGHVLTDFGLCKEVEPDTTSTFCGTEYLAPEVLHKOPYDRYVDM 277
 QY 295 WCLGAVLYEMLYGLPPFYSRNTAEYDNLNKLQKPNITNSARHLEGLLQKDRTKRL 354
 DB 278 WCLGAVLYEMLYGLPPFYSDVQMYENILHQPLOIPGGRVAAACDLQSLHKKDQRL 337
 QY 355 GAKODFMEIKSHVFFSLINWDDLKNTTPPNPNVSCPNDLRHFDEFTPEEPNPSIGK 414
 DB 338 GSKADFELEIKNHVFFSPINWDDLKRLTTPFPNPNVTGPADLKHDFDEFTQEAVSKSIGC 397
 QY 415 SPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
 DB 398 TPTVT---ASSGASSAFLGFSYAPEDDDIL 425

RESULT 9

Q9UKG6 PRELIMINARY; PRT; 367 AA.
 AC Q9UKG6
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Protein kinase (DJI1387.2) (Serum/glucocorticoid regulated kinase 2)
 DE (Similar to serum/glucocorticoid regulated kinase 2).
 GN SGK2ALPHA OR SGK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20018032; PubMed=10548550;
 RA Kobayashi T., Deak M., Morrice N., Cohen P.;
 RT "Characterization of the structure and regulation of two novel
 RT isoforms of serum- and glucocorticoid-induced protein kinase.";
 RL Biochem. J. 344:189-197(1999).
 DR EMBL; AF186470; AAG17012.1; -.
 DR HSSP; P05132; IATP.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase C; 1.
 RP SEQUENCE FROM N.A.
 RA Ramsay H.;
 RN Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RN [3]
 RP SEQUENCE FROM N.A.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AF169034; AAF12757.2; -.
 DR EMBL; BC014037; AAC18509.1; -.
 DR EMBL; Z98752; CAC18509.1; -.
 DR HSSP; P05132; IATP.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase C; 1.

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DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TK_X; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00109; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00110; PROTEIN KINASE ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 367 AA; 41174 MW; E53FIABE253F648B CRC64;
SQ

Query Match 60.3%; Score 1411; DB 4; Length 367;
Best Local Similarity 71.2%; Pred. No. 2.3e-108;
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;

Qy 83 MNANP--SPPPSPSQ---QINLGSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVF 137
Db 1 MNSSPAGTSPQPSGRANGNINLGSPANPNARPTDFDLKVIKGNKGYKVLAKRSDGAF 60
Qy 138 YAVVLQKATLKKEEKHIMSERVLLKNVHPFLVGLHFSFOTADKLYFVLDYINGGE 197
Db 61 YAVVLQKSKLKKEESHIMSERVLLKNVHPFLVGLHFSFOTADKLYFVLDYINGGE 120
Qy 198 LFYHLQRCFLPRARFYAAEIASALGYLHSLNIVRDLPENILLDSQGHIVLTDPL 257
Db 121 LFFHLQRRFLPRARFYAAEIASALGYLHSLNIVRDLPENILLDSQGHIVLTDPL 180
Qy 258 CKEIEHNSTSTSCGTPPEYLAPVLRKQPYDRTVDMWCLGAVLYEMLYGLPPYSNTA 317
Db 181 CKEGVEPEDTSTSCGTPPEYLAPVLRKQPYDRTVDMWCLGAVLYEMLYGLPPYSQDVS 240
Qy 318 EYDNILNKLQPKNTNSARHLLGLLQKDRKLGAKDDFMEIKSHVFFSLINWDDL 377
Db 241 QYENILHQPLOIPGGRTVAACDLQLSLHDKQRLGSKADFLKIHVFFSPINWDDL 300
Qy 378 INKKTTPFPNVSQNDLRFDEFTPEEPVNSIGKSPSVLTASVKEAAEAFLGFSY 437
Db 301 YHKRLTPFPNVTGADLKHDFEFTQEAIVSKSIGCTPTDV---ASSSGASSAFLGFSY 357
Qy 438 APPTDSFL 445
Db 358 APEDDDIL 365

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RESULT 10
Q9QZ55 ID Q9QZ55 PRELIMINARY; PRT; 367 AA.
AC Q9QZ55;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Protein kinase.
GN SGK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20018032; PubMed=10548550;
RA Kobayashi T., Deak M., Morrice N., Cohen P.;
RT "Characterization of the structure and regulation of two novel
RT isoforms of serum- and glucocorticoid-induced protein kinase.";
RL Biochem. J. 344:189-197 (1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF169033; AAF12756.1; -.
DR HSSP; P05132; 1CTP.
DR MGD; MGI:1351318; SGK2.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Euk_pkinase; 1.

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DR SMART; SM00220; S_TK_X; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00109; PROTEIN KINASE ATP; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 367 AA; 41359 MW; 668C04B1A1E9E33A CRC64;
SQ

Query Match 59.3%; Score 1387; DB 11; Length 367;
Best Local Similarity 71.1%; Pred. No. 2.2e-106;
Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;

Qy 87 PPSPPSPSQ-QINLGSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVFYAVKVLQK 145
Db 9 PPSQPSRANGNINLGSPANPNARPTDFDLKVIKGNKGYKVLAKRSDGAFYAVKVLQK 68
Qy 146 KAILKKKEKHIMSERVLLKNVHPFLVGLHFSFOTADKLYFVLDYINGGELFYHLQRE 205
Db 69 KSLKKNKQNHIMAEARNVLLKNVHPFLVGLRYSFOTPEKLYFVLDYVNGGELFFHLQRE 128
Qy 206 RCLEPRARFYAAEIASALGYLHSLNIVRDLPENILLDSQGHIVLTDPLGCKENIEHN 265
Db 129 RRELEPRARFYAAEIASALGYLHSLNIVRDLPENILLDSQGHIVLTDPLGCKECVEPE 188
Qy 266 STTSTFCGTPPEYLAPVLRKQPYDRTVDMWCLGAVLYEMLYGLPPYSNTAEMYDNLN 325
Db 189 ETTSTFCGTPPEYLAPVLRKQPYDRTVDMWCLGAVLYEMLYGLPPFNTDVAQMYENILH 248
Qy 326 KPIQLKPNITNSARHLLGLLQKDRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPP 385
Db 249 QPLQIPGRTVAACDLQLSLHDKQRLGSKEDFLDKNHMFSPINWDDLHYKRLTTP 308
Qy 386 FNPVNSQNDLRFDEFTPEEPVNSIGKSPSVLTASVKEAAEAFLGFSYAPPTDSFL 445
Db 309 FNPVNSQNDLRFDEFTPEEPVNSIGKSPSVLTASVKEAAEAFLGFSYAQDDDDIL 365

RESULT 11
Q8ROP6 ID Q8ROP6 PRELIMINARY; PRT; 366 AA.
AC Q8ROP6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Serum/glucocorticoid regulated kinase 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026549; AAH26549.1; -.
KW Kinase.
SQ SEQUENCE 366 AA; 41231 MW; D6786996069EF3F4 CRC64;

Query Match 58.7%; Score 1374.5; DB 11; Length 366;
Best Local Similarity 71.1%; Pred. No. 2.4e-105;
Matches 256; Conservative 50; Mismatches 49; Indels 5; Gaps 3;

Qy 87 PPSPPSPSQ-QINLGSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVFYAVKVLQK 145
Db 9 PPSQPSRANGNINLGSPANPNARPTDFDLKVIKGNKGYKVLAKRSDGAFYAVKVLQK 68
Qy 146 KAILKKKEKHIMSERVLLKNVHPFLVGLHFSFOTADKLYFVLDYINGGELFYHLQRE 205
Db 69 KSLKKNK-ENHIMAEARNVLLKNVHPFLVGLRYSFOTPEKLYFVLDYVNGGELFFHLQRE 127
Qy 206 RCLEPRARFYAAEIASALGYLHSLNIVRDLPENILLDSQGHIVLTDPLGCKENIEHN 265
Db 128 RRELEPRARFYAAEIASALGYLHSLNIVRDLPENILLDSQGHIVLTDPLGCKECVEPE 187

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QY 266 STTSTFCGTEYLAEVHLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLN 325
 DB 188 ETTSTFCGTEYLAEVHLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLN 247
 QY 326 KPLQKRNITNSARHLLEGILQKQRTKRLGAKDDFMEIKSHVFSNLNWDLLINKKITPP 385
 DB 248 QPQIPGRTVAACDLQGLLHKDQRLGSKEDFLDKNHMFSPINWDDLHKRLTTP 307
 QY 386 FPNVSGPDLRHFDPTEEPENSGIKSPDSVLVTASVKEAAEAPLGFSAAPPTDSFL 445
 DB 308 FPNVEGPADLKHDFDEFTQENSVKSGCTPDTV--ASSGASAFGLFSYAQDDDDIL 364

RESULT 12
 Q8R4U9 ID Q8R4U9 PRELIMINARY; PRT; 302 AA.
 AC Q8R4U9
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE Serum- and glucocorticoid-inducible kinase 2-related (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN RN
 RC SEQUENCE FROM N.A.
 RP STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;
 RA Feng Y.X., Huber S.M., Waerniges S., Lang F.;
 RT "SGK2 and SGK3 mRNA expression in rat kidney.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF361756; AAL91351.1;
 KW Kinase.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 302 AA; 34622 MW; A74EE3F424283D66 CRC64;

Query Match 52.8%; Score 1236; DB 11; Length 302;
 Best Local Similarity 74.0%; Pred. No. 5.1e-94;
 Matches 222; Conservative 45; Mismatches 33; Indels 0; Gaps 0;

QY 97 INLGPSNPHAKPSDFHLKVIKSGFGKVLARHKAEEVYAVKVLQKAILKKEKH 156
 DB 3 INLGPSANPNARPTDFDLKVIKSGYKGVLLAKRSDGAFYAVKVLQKAILKKEQH 62
 QY 157 IMSENVLLKNVHPFLVGLHFSFQADKLYFVLDYINGGELFYHLQRECFLEPRFY 216
 DB 63 IMAEVNLKNVHPFLVGLHFSFQADKLYFVLDYINGGELFYHLQRECFLEPRFY 122
 QY 217 AAEIASALGYLHSLNIVYRDLKPNILLDSQGHVLTDFGLCKENIEHNSTTSTFCGTP 276
 DB 123 TAEVASAIGYLSLNIYRDLKPNILLDCQGHVLTDFGLCKEVEPEETSTFCGTP 192
 QY 277 YLAPEVHLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKLKPNITN 336
 DB 183 YLAPEVHLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKLKPNITN 242
 QY 337 SARHLEGILQKQRTKRLGAKDDFMEIKSHVFSNLNWDLLINKKITPPENNVSGNDL 396
 DB 243 AACDLQGLLHKDQRLGSKEDFLDKNHMFSPINWDDLHKRLTTPFPNVEGPADL 302

RESULT 13
 Q94365 ID Q94365 PRELIMINARY; PRT; 422 AA.
 AC Q94365;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DE Serum- and glucocorticoid-inducible kinase 2-related (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN RN
 RC SEQUENCE FROM N.A.
 RP STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;
 RA Feng Y.X., Huber S.M., Waerniges S., Lang F.;
 RT "SGK2 and SGK3 mRNA expression in rat kidney.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF361756; AAL91351.1;
 KW Kinase.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 302 AA; 34622 MW; A74EE3F424283D66 CRC64;

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN RN
 RP SEQUENCE FROM N.A.
 RA McMuray A.A.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; Z81140; CAB03485.1;
 DR HSSP; P05132; IATP.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00133; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00107; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR ATP-binding; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 422 AA; 49672 MW; 1FA75EF677B88C00 CRC64;

Query Match 46.2%; Score 1082; DB 5; Length 422;
 Best Local Similarity 52.0%; Pred. No. 4.3e-81;
 Matches 204; Conservative 71; Mismatches 99; Indels 18; Gaps 4;

QY 32 ESFLLSGLAFMKQRRMGLNDFQKIANNYSACKHPEVQSLKISQOEPELMANPSPPP 91
 DB 29 KKFQADSKFEYKRRVWILVISQHLVDNN--LRSEDEVRRFFHLESPPDDE----- 76
 QY 92 SPSQQLNGLPSSNPHAKPSDFHLKVIKSGFGKVLARHKAEEVYAVKVLQKAILKK 151
 DB 77 ---NVLDLSPERKATANDFDYLTITIGKSGFQVYQVRHETKTIYAMKILSKHIRKK 133
 QY 152 KEEKHIMSERNVLLKNVHPFLVGLHFSFQADKLYFVLDYINGGELFYHLQRECFLEP 211
 DB 134 NEVGHVMAERNVLLNFKHPFLVGLHFSFQADKLYFVLDHNGELFYHLQRECFLEP 193
 QY 212 RARFYAAETASALGYLHSLNIVYRDLKPNILLDSQGHVLTDFGLCKENIEHNSTTSTF 271
 DB 194 RSRFYAAETASALGYLHSLNIVYRDLKPNILLDSQGHVLTDFGLCKEDMQCKTTSTF 253
 QY 272 CGTPEYLAPEVHLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKLK 331
 DB 254 CGTPEYLAPEVHLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKLK 313
 QY 332 PNITNSARHLLEGILQKQRTKRLGAKDDFMEIKSHVFSNLNWDLLINKKITPPFNPNV 391
 DB 314 HNISVPCSELIITGLQKQSKRLGHRNDFRDPHFFLPVDMWDLNKLKXAPFIPKVK 373
 QY 392 GPNDRHFDPTEEPV-PNSIGKSPDSVLVT 422
 DB 374 NAMDTSNISKEFVEIQIDPSSL--APQLAVT 403

RESULT 14
 Q99LU4 ID Q99LU4 PRELIMINARY; PRT; 185 AA.
 AC Q99LU4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE Similar to serum/glucocorticoid regulated kinase (Fragment).
 DE SGK.
 GN SGK.

OS Mus musculus (Mouse)
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC002222; AH02222.1; -
 DR MGD; MGI:1340062; Sgk.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase; C; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00133; S_TK X; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Kinase
 FT NON_TER
 SQ SEQUENCE 185 AA; 20921 MW; EDAA44ABF083945 CRC64;
 Query Match 40.6%; Score 951; DB 11; Length 185;
 Best Local Similarity 96.1%; Pred. No. 9.3e-71;
 Matches 174; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 265 NNTSTTCGTPPEYLAPEVLHQPYDRVTDMWCLGAVLYEMLYGLPPFYGRNTAEYDNL 324
 Db 5 NGTSTTCGTPPEYLAPEVLHQPYDRVTDMWCLGAVLYEMLYGLPPFYGRNTAEYDNL 64
 QY 325 NKPLQKPNITNSARHLLEGLOKDRTRIGAKDMEIKSHVFFSLINWDDLINKKITP 384
 Db 65 NKPLQKPNITNSARHLLEGLOKDRTRIGAKDMEIKSHVFFSLINWDDLINKKITP 124
 QY 385 PFNPVNSGPNDLRHFDPEFTTEEPVNSIGKSPDSVLVTASVKAEAAFLGFSYAPPTDSF 444
 Db 125 PFNPVNSGPNDLRHFDPEFTTEEPVNSIGKSPDSVLVTASVKAEAAFLGFSYAPPVDSF 184
 QY 445 L 445
 Db 185 L 185
 RESULT 15
 Q96QV3 PRELIMINARY; PRT; 465 AA.
 AC Q96QV3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Protein Kinase B gamma 1.
 GN AKT3.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11387345;
 RA Brodbeck D., Hill M.M., Hemmings B.A.;
 RT "Two Splice Variants of Protein Kinase B gamma Have Different
 RT Regulatory Capacity Depending on the Presence or Absence of the
 RT Regulatory Phosphorylation Site Serine 472 in the Carboxyl-terminal
 RT Hydrophobic Domain."
 RL J. Biol. Chem. 276:29550-29558(2001).
 DR ENBL; AY005799; AAF91073.1; -
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR *Pfam; PF00169; PH; 1.

DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; Pkinase C; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
 KW ATP-binding; Kinase; Transferase;
 SQ SEQUENCE 465 AA; 54032 MW; 592EF8B86937D1E0 CRC64;
 Query Match 39.0%; Score 912; DB 4; Length 465;
 Best Local Similarity 47.0%; Pred. No. 5.4e-67;
 Matches 167; Conservative 63; Mismatches 120; Indels 28; Gaps 7;
 QY 33 SFLLSGLAFMKQRRMGLNDFIOK-----IANNSTACKHPE-----VQSILKISQSQ 78
 Db 53 NFSVAKCQLMKTERPKPNTFIIRCLQWTTVIERTFHVDTPEREETEAIAQVADRLORQ 112
 QY 79 EPELNANPSPPPSPSQINLG---PSSNPHAK---PSDFHLKVIKSGFGKVLARH 131
 Db 113 EBERMNCST-----SQDNI GEEEMDASTTHHKRTMWDFFYLKLGKGTGKVLIVRE 167
 QY 132 KAEVEFYAVKVLQKAILKKKEEKHIMSERNVLLKNVHPFLVGLHFSFQTADKLYFVLD 191
 Db 168 KASGKYAMKILKKEVIAKDEVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVME 226
 QY 192 YINGGELFVHLORECRFCLEPRARFYAAETASALGYLHSLNIVYRDLKPNILLDSOGHIV 251
 Db 227 YVNGGELFPHLSRERVFESDRTRFYCAETVSALDYLSHGKI VYRDLKLENLMLDKDGHK 286
 QY 252 LTDFGLCKENIEHNSTSTFCGTPEYLAPEVLHQPYDRVTDMWCLGAVLYEMLYGLPPF 311
 Db 287 ITDFGLCKEGITDAATMTKTCGTPEYLAPEVLEDDNDYGRAVDWGLGVVYENWMCGRLPF 346
 QY 312 YSRNTAEYDNLINKPLQKPNITNSARHLLEGLOKDRTRIGAKDMEIKSHVFFS 370
 Db 347 YNQDHEKLPFLIMEDIKFPRTLSSDAKSLLSGLLIKDPNKLKLGSGPDDAKEIMRHSFFS 406
 QY 371 LINWDDLINKKITPPFPNPVNSGPNDLRHFDPEFTTEEPV 408
 Db 407 GVNWQDVYDKLVPFPKQVTSSETDTRYDEEFTAQTI 444
 Search completed: June 20, 2003, 19:26:46
 Job time : 85 secs

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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:15:08 ; Search time 22 Seconds
(without alignments)
838.953 Million cell updates/sec

Title: US-10-067-977-2

Perfect score: 2340

Sequence: 1 MGENQALARLESLLRPR.....KEAAEFLGFSYAPPTDSDL 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2150	91.9	431	1	SGK_HUMAN
2	2111	90.2	431	1	SGK_RABIT
3	2107	90.0	431	1	SGK_MOUSE
4	2100.5	89.8	430	1	SGK_RAT
5	916	39.1	479	1	AKT3_HUMAN
6	916	39.1	479	1	AKT3_MOUSE
7	910	38.9	454	1	AKT3_RAT
8	878	37.5	480	1	KRAC_RAT
9	878	37.5	501	1	KAKT_MLVAT
10	876	37.4	480	1	KRAC_MOUSE
11	864.5	36.9	479	1	PK2_DICDI
12	863.5	36.9	481	1	AKT2_HUMAN
13	862	36.8	480	1	KRAC_BOVIN
14	861.5	36.8	481	1	AKT2_MOUSE
15	861	36.8	480	1	KRAC_HUMAN
16	857	36.6	444	1	KRAC_DICDI
17	852.5	36.4	481	1	AKT2_RAT
18	831.5	35.5	677	1	YPK2_YEAST
19	827.5	35.4	680	1	YPK1_YEAST
20	816	34.9	485	1	K6B2_MOUSE
21	810.5	34.6	482	1	K6B2_HUMAN
22	807	34.5	502	1	K6B1_HUMAN
23	807	34.5	502	1	K6B1_RAT
24	799	34.1	634	1	KPC3_DROME
25	796.5	34.0	1016	1	PKC2_SCHPO
26	791.5	33.8	672	1	KPCA_HUMAN
27	791.5	33.8	672	1	KPCA_RAT
28	791.5	33.8	743	1	KPC2_APLCA
29	790.5	33.8	672	1	KPCA_RABIT
30	789.5	33.7	672	1	KPCA_BOVIN
31	784.5	33.5	649	1	KPC1_APLCA
32	784	33.5	671	1	KPCB_HUMAN
33	783	33.5	671	1	KPCB_MOUSE

34 783 33.5 671 1 KPCB_RABIT P05772 oryctolagus
35 781 33.4 707 1 KPC2_CABEL P34885 caenorhabdi
36 780.5 33.4 672 1 KPCA_MOUSE P20444 mus musculu
37 779.5 33.3 988 1 PKC1_SCHPO P36582 schizosacch
38 778.5 33.3 737 1 KPCF_MOUSE P16054 mus musculu
39 776 33.2 696 1 SCK1_SCHPO P50530 schizosacch
40 776 33.2 737 1 KPCF_HUMAN Q02156 homo sapien
41 774.5 33.1 587 1 KPCI_HUMAN P41743 homo sapien
42 772.5 33.0 736 1 KPCI_MOUSE Q62074 mus musculu
43 772.5 33.0 736 1 KPCF_RABIT P10830 oryctolagus
44 767 32.8 682 1 KPCG_BOVIN P05128 bos taurus
45 765 32.7 658 1 KPCI_LYPTI Q25378 lytechinus

ALIGNMENTS

RESULT 1
SGK_HUMAN
ID SGK_HUMAN STANDARD; PRT; 431 AA.
AC O00141; Q9UN56;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase Sgk (EC 2.7.1.-)
DE (Serum/glucocorticoid-regulated kinase).
GN SGK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97272242; PubMed=9114008;
RA Waldegger S., Barth P., Raber G., Lang F.;
RT "Cloning and characterization of a putative human serine/threonine
RT protein kinase transcriptionally modified during anisotonic and
RT isotonic alterations of cell volume.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4440-4445(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98390195; PubMed=9722955;
RA Waldegger S., Erdel M., Nagl U.O., Barth P., Raber G., Steuer S.,
RA Utermann G., Paulmichl M., Lang F.;
RT "Genomic organization and chromosomal localization of the human SGK
RT protein kinase gene.";
RL Genomics 51:299-302(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Kim M.K., Kim Y.H., Seo J.M., Lee H.M., Chung H.J., Sohn M.Y.,
RA Hwang S.Y., Im S.U., Jung E.J., Kim J.C.;
RT "A catalogue of genes in the human dermal papilla cells as identified
RT by expressed sequence tags.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT TISSUE=Cervix;
CC Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLE PROTEIN KINASE THAT MAY ACT IN RENAL EPITHELIA
CC TO ACTIVATE APICAL SODIUM CHANNELS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC
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CC
DR EMBL; Y10032; CAA71138.1; -.
DR EMBL; AJ000512; CAA04146.1; -.

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DR EMBL; AF153609; AAD41091.1; -.
DR EMBL; BC001263; AAOH1263.1; -.
DR HSP; P00517; 1YDR.
DR Genew; HGNC:10810; SGK.
DR MIM; 602958; -.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00110; PROTEIN_KINASE_DOM; 1.
DR TRANSFERASE; Serine/threonine-protein kinase; ATP-binding.
KW DOMAIN 98 355 PROTEIN_KINASE.
FT NP BIND 104 112 ATP (BY SIMILARITY).
FT BINDING 127 127 ATP (BY SIMILARITY).
FT ACT SITE 222 222 BY SIMILARITY.
FT CONFLICT 381 381 E -> D (IN REF. 3 AND 4).
SQ SEQUENCE 431 AA; 48956 MW; F3697DA57073399D CRC64;

Query Match 91.9%; Score 2150; DB 1; Length 431;
Best Local Similarity 99.5%; Pred. No. 3.7e-143;
Matches 405; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 39 LAFMKQRRMGLNDFIQKIANNYSYACKHPEVQSILKISQPEPELMNANPPSPSQOIN 98
Db :|||||
Db 25 IAFMKQRRMGLNDFIQKIANNYSYACKHPEVQSILKISQPEPELMNANPPSPSQOIN 84
Qy 99 LGPSSNPHAKPSDFHFLKVGKSGFKVLLARHKAEEVFYAVKVLQKAILKKKEKHIM 158
Db :|||||
Db 85 LGPSSNPHAKPSDFHFLKVGKSGFKVLLARHKAEEVFYAVKVLQKAILKKKEKHIM 144
Qy 159 SERNVLLKNVGHPLVGLHFSFQTADKLYFVLDYINGGELFYHLQRECFLEPRARYAA 218
Db :|||||
Db 145 SERNVLLKNVGHPLVGLHFSFQTADKLYFVLDYINGGELFYHLQRECFLEPRARYAA 204
Qy 219 ETASALGYLHSLNIVYRDLPENILDSQGHIVLTDGLCKENIEHNSTTSTFCGTPEYL 278
Db :|||||
Db 205 ETASALGYLHSLNIVYRDLPENILDSQGHIVLTDGLCKENIEHNSTTSTFCGTPEYL 264
Qy 279 APEVLHKQPYDRTVDWCLGAVLYEMLYGLPPFYSRNTAEYDNLKPLQKPNITNSA 338
Db :|||||
Db 265 APEVLHKQPYDRTVDWCLGAVLYEMLYGLPPFYSRNTAEYDNLKPLQKPNITNSA 324
DE (Serine/threonine-protein kinase Sgk (EC 2.7.1.-))
DE (Serum/glucocorticoid-regulated kinase).
GN SGK.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Legomorphia; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.

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RESULT 2

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SGK_RABIT
ID - SGK_RABIT STANDARD; PRT; 431 AA.
AC Q9XT18;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE (Serine/threonine-protein kinase Sgk (EC 2.7.1.-))
DE (Serum/glucocorticoid-regulated kinase).
GN SGK.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Legomorphia; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=New Zealand white;
RX MEDLINE=99287894; PubMed=10358046;
RA Naray-Fejes-Toth A., Canessa C., Cleaveland E.S., Aldrich G.,
RA Fejes-Toth G.;
RT "sgk is an aldosterone-induced kinase in the renal collecting duct.
RT Effects on epithelial Na+ channels.";
RL J. Biol. Chem. 274:16973-16978(1999).
CC -I- FUNCTION: PROBABLE PROTEIN KINASE THAT MAY ACT IN RENAL EPITHELIA
CC TO ACTIVATE APICAL SODIUM CHANNELS.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF139639; AAD43303.1; -.
DR HSP; P00517; 1YDR.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00110; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 98 355 PROTEIN_KINASE.
FT NP BIND 104 112 ATP (BY SIMILARITY).
FT BINDING 127 127 ATP (BY SIMILARITY).
FT ACT SITE 222 222 BY SIMILARITY.
SQ SEQUENCE 431 AA; 48999 MW; 354898A77B8E38FD CRC64;

Query Match 90.2%; Score 2111; DB 1; Length 431;
Best Local Similarity 97.1%; Pred. No. 1.9e-140;
Matches 395; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 39 LAFMKQRRMGLNDFIQKIANNYSYACKHPEVQSILKISQPEPELMNANPPSPSQOIN 98
Db :|||||
Db 25 IAFMKQRRMGLNDFIQKIANNYSYACKHPEVQSILKISQPEPELMNANPPSPSQOIN 84
Qy 99 LGPSSNPHAKPSDFHFLKVGKSGFKVLLARHKAEEVFYAVKVLQKAILKKKEKHIM 158
Db :|||||
Db 85 LGPSSNPHAKPSDFHFLKVGKSGFKVLLARHKAEEVFYAVKVLQKAILKKKEKHIM 144
Qy 159 SERNVLLKNVGHPLVGLHFSFQTADKLYFVLDYINGGELFYHLQRECFLEPRARYAA 218
Db :|||||
Db 145 SERNVLLKNVGHPLVGLHFSFQTADKLYFVLDYINGGELFYHLQRECFLEPRARYAA 204
Qy 219 ETASALGYLHSLNIVYRDLPENILDSQGHIVLTDGLCKENIEHNSTTSTFCGTPEYL 278
Db :|||||
Db 205 ETASALGYLHSLNIVYRDLPENILDSQGHIVLTDGLCKENIEHNSTTSTFCGTPEYL 264
Qy 279 APEVLHKQPYDRTVDWCLGAVLYEMLYGLPPFYSRNTAEYDNLKPLQKPNITNSA 338
Db :|||||
Db 265 APEVLHKQPYDRTVDWCLGAVLYEMLYGLPPFYSRNTAEYDNLKPLQKPNITNSA 324
Qy 339 RHLEGLLQKDRTKRLGAKDDFMFKSHVFFSLINWDDLKINKITPPFPNVSGPNDLRH 398
Db :|||||
Db 325 RHLEGLLQKDRTKRLGAKDDFMFKSHVFFSLINWDDLKINKITPPFPNVSGPNDLRH 384
Qy 399 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEALFGFSYAPPTDSFL 445
Db :|||||
Db 385 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEALFGFSYAPPTDSFL 431

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RESULT 3
SGK_MOUSE
ID - SGK_MOUSE STANDARD; PRT; 431 AA.
AC Q9WVC6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase Sgk (EC 2.7.1.-)
DE (Serum/glucocorticoid-regulated kinase).
DE SGK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=99287894; PubMed=103580046;
RA Naray-Fejes-Toth A., Canessa C., Cleaveland E.S., Aldrich G.,
RA Fejes-Toth G.;
RT "sgk is an aldosterone-induced kinase in the renal collecting duct.
RT Effects on epithelial Na+ channels.";
RL J. Biol. Chem. 274:16973-16978(1999).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=20215285; PubMed=10751222;
RA Shigaev A., Asher C., Latter H., Garty H., Reuveny E.;
RT "Regulation of sgk by aldosterone and its effects on the epithelial
RT Na(+) channel.";
RL Am. J. Physiol. 278:F613-F619(2000).
CC -1- FUNCTION: PROBABLE PROTEIN KINASE THAT MAY ACT IN RENAL EPITHELIA
CC TO ACTIVATE APICAL SODIUM CHANNELS.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
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CC -----
DR ENBL; AF139638; AAD43302.1; -.
DR EMBL; AF205855; AAF19429.1; -.
DR HSP: P00517; IYDR
DR HSD: MGI:1340062; Sgk.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase.1.
DR Pfam; PF00433; pkinase.C; 1.
DR PRINTS; P00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; _PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; _PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; _PROTEIN_KINASE_ST; 1.
DR Transfaser; Serine/threonine-protein kinase; ATP-binding.
KW DOMAIN 98 355 PROTEIN KINASE.
FT NP BIND 104 112 ATP (BY SIMILARITY).
FT BINDING 127 127 ATP (BY SIMILARITY).
FT ACT SITE 222 222 BY SIMILARITY.
SQ SEQUENCE 431 AA; 49928 MW; 6DF5B8464A4C2754 CRC64;
Query Match 90.0%; Score 2107; DB 1; Length 431;
Best Local Similarity 93.0%; Pred. No. 3.7e-140;
Matches 398; Conservative 13; Mismatches 12; Indels 6; Gaps 1;
QY 24 RAFAQK-----RSEFLLSGLAFMKQRRMGLNDFTQKIANNYSACKHPVQSILKISQP 77
Db 4 KAEAAESTLTYSMRGMVAIIAFMKQRRMGLNDFIQKIASNTYACKHAEVQSIKMSHP 63

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QY	371	LINWDLINKITPPNPVNSGVNDLRHFDPEFTTEEPVPNSIGKSPDSVLVTASVKAAE	430
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Db	407	GNVNQVDYDKLVPPKPQVTSSETDTRYFDEEFTAQTITTPPEKYDDGMDCMONERRP	466
QY	431	AFLGFESYA	438
	:	: :: : : :	:
Db	467	HFPQFSYS	474

RESULT 6
ACT3_MOUSE

ID	ACT3_MOUSE	STANDARD;	PRT;	479 AA.
AC	Q9WU6;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DT	RAC-gamma serine/threonine protein kinase [EC 2.7.1.-] (RAC-PK-gamma)			
DE	(Protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma).			
GN	AKT3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCEI_TaxID=10090;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=99194749; PubMed=10092583;			
RX	Brodbeck D., Cron P., Hemmings B.A.;			
RA	"A human protein kinase B gamma with regulatory phosphorylation sites			
RT	in the activation loop and in the C-terminal hydrophobic domain.";			
RL	J. Biol. Chem. 274:9133-9136(1999).			
RL	[2]			
RC	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Brain;			
RX	PubMed=11387345;			
RA	Brodbeck D., Hill M.M., Hemmings B.A.;			
RT	"Two splice variants of PKB gamma have different regulatory capacity			
RT	depending on the presence or absence of the regulatory phosphorylation			
RT	site Ser 472 in the C-terminal hydrophobic domain.";			
RL	J. Biol. Chem. 276:29550-29558(2001).			
CC	-1- FUNCTION: IGF-1 LEAD TO THE ACTIVATION OF AKT3, WHICH MAY PLAY A			
CC	ROLE IN REGULATING CELL SURVIVAL. CAPABLE OF PHOSPHORYLATING			
CC	SEVERAL KNOWN PROTEINS. TRUNCATED ISOFORM 2/PKB GAMMA 1 WITHOUT			
CC	THE SECOND SERINE PHOSPHORYLATION SITE COULD STILL BE STIMULATED			
CC	BUT IN A LESSER EXTENT (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-ASSOCIATED AFTER			
CC	CELL STIMULATION LEADING TO ITS TRANSLOCATION.			
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/PKB GAMMA (SHOWN HERE) AND			
CC	2/PKB GAMMA 1; ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- TISSUE SPECIFICITY: ISOFORM 1 IS EXPRESSED IN PROSTATE, TESTIS,			
CC	UTERUS AND MAMMARY GLAND AND ISOFORM 2 IS EXPRESSED IN PROSTATE,			
CC	TESTIS AND MAMMARY GLAND.			
CC	-1- DOMAIN: BINDING OF THE PH DOMAIN TO THE PHOSPHATIDYLINOSITOL 3-			
CC	KINASE ALPHA (PI(3)K) RESULTS IN ITS TARGETING TO THE PLASMA			
CC	MEMBRANE.			
CC	-1- PTM: PHOSPHORYLATED ON THREONINE AND SERINE RESIDUES.			
CC	PHOSPHORYLATION ON BOTH SITES IS REQUIRED FOR FULL ACTIVITY.			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	RAC SUBFAMILY.			
CC	-1- SIMILARITY: CONTAINS 1 PH DOMAIN.			
CC	-----			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF124142; AAC29090.1; -			
DR	HSSP; P05132; ICTP.			
DR	MGI; MG11345147; Akt3.			
DR	InterPro; IPR000719; Euk pkKinase.			

[illegible]

RESULT 7			
AKT3-RAT			
ID	AKT3	RAT	
AC	Q63484;		
DT	16-OCT-2001	(Rel. 40, Created)	
DT	16-OCT-2001	(Rel. 40, Last sequence update)	
DT	16-OCT-2001	(Rel. 40, Last annotation update)	

RAC-gamma serine/threonine protein kinase (EC 2.7.1.-) (RAC-PK-gamma)
 (protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma).
 AKT3.
 Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP
 RS TISSUE=Brain;
 RC MEDLINE=96063640; PubMed=7488143;
 RX Konishi H., Kuroda S., Tanaka M., Matsuzaki H., Ono Y., Kanezawa K.,
 RA Haga T., Kikkawa U.;
 RT "Molecular cloning and characterization of a new member of the RAC
 RT protein kinase family; association of the pleckstrin homology domain
 RT of three types of RAC protein kinase with protein kinase C subspecies
 RT and beta gamma subunits of G proteins.";
 RL Biochem. Biophys. Res. Commun. 216:526-534(1995).
 CC -!- FUNCTION: IGF-1 LEAD TO THE ACTIVATION OF AKT3, WHICH MAY PLAY A
 CC ROLE IN REGULATING CELL SURVIVAL. CAPABLE OF PHOSPHORYLATING
 CC SEVERAL KNOWN PROTEINS (BY SIMILARITY).
 CC -!- DOMAIN: BINDING OF THE PH DOMAIN TO THE PHOSPHATIDYLINOSITOL 3-
 CC KINASE ALPHA (PI(3)K) RESULTS IN ITS TARGETING TO THE PLASMA
 CC MEMBRANE.
 CC -!- PTM: PHOSPHORYLATED ON THREONINE AND SERINE RESIDUES.
 CC PHOSPHORYLATION ON BOTH SITES IS REQUIRED FOR FULL ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. RAC
 CC SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.

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 or send an email to license@isb-sib.ch).

 ENBL; D49836; BAA08637.1; --
 DR HSSP; P05132; IFMO.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000961; pkinase_C.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00133; S-TK_X; 1.
 DR SMART; SM00220; S-TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PSS0003; PH_DOMAIN; 1.
 DR PROSITE; PS10011; PROTEIN_KINASE_DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 Phosphorylation.
 KM
 FT DOMAIN 5 107 PH.
 FT DPAIN 148 405 PROTEIN_KINASE.
 FT NP_BIND 154 162 ATP (BY SIMILARITY).
 FT BINDING 177 177 ATP (BY SIMILARITY).
 FT ACT_SITE 271 271 BY SIMILARITY.
 FT MOD_RES 305 305 PHOSPHORYLATION (BY SIMILARITY).
 SO SEQUENCE 454 AA; 52849 MW; 6B072CFF9DEE876 CRC64;

```

Query Match          38.9%; Score 910; DB 1; Length 454;
Best Local Similarity 47.0%; Pred. No. 1.7e-56;
Matches 187; Conservative 63; Mismatches 120; Indels 28; Gaps 7
Qy 33 SFLSLGLAFKQRRMGMLNDRIQK-----IANNSYACKHPK-----VOSILKISQPQ 78
Db 53 NFSVAKCOLMKTERPKNTIIIRCLQWTVIERTFHVDTPEEREWEATEAIQAVADRQQR 112

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Qy 79 EPELMANPPSPSPSQINLG-----PSSNPFAK---PSDFHFLKVIKSGFGKVLARH 131
Db 113 EERNMNSPT-----SOLDNIGEEEMASTTHHRKRTMNDYDLKLGKGTGKVLVRE 167
Qy 132 KAEEVFVAVKQKAILKKKEEKHINSERNVLKNVKKHPFLVGLHFSFQTADKLYFVLD 191
Db 168 KASGYAMKILKEVIAKDEVAHTITESRV-LKNTRHPLTSLKTSFQTKRLCFVME 226
Qy 192 YINGELFYHLQRCFLPRARYAAIASALGYLHSLNIVYRDLPENILLDSOGHIV 251
Db 227 YVNGELFFHLRSRVSFSDRTREYGAIVSALDYLSHGKIVYRDLPENILLDSOGHIV 286
Qy 252 LTDFGLCKENIEHNSITSTFCGTEYLAPVHLKQPDRTVDWCLGAVLYEMLYGLPPP 311
Db 287 ITDFGLCKEGITDAATWKTCGTEYLAPVHLKQPDRTVDWCLGAVLYEMLYGLPPP 346
Qy 312 YSRNTAEMYNILNKPLQKNPNTNSARHLLGLELQKDRKRL-GAKDDFMFEIKSHVFFS 370
Db 347 YNQDHEKLPFELLMEDIKFRTLSSDAKSLLSGLLIIDPNKRLGGGDDPKKEIMRHSFFS 406
Qy 371 LINWDDLINKKITPPFNPVNSGPNDRHFDPEFTEEPV 408
Db 407 GVNQDVYDKLVPPFKPQVTSSETDTRYFDEEFTAQTI 444

RESULT 8
KRAC RAT
ID KRAC RAT STANDARD; PRT; 480 AA.
AC P47196; 1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE RAC-alpha serine/threonine kinase (EC 2.7.1.-) (RAC-PK-alpha)
DE (protein kinase B) (PKB).
GN AKT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=95091823; PubMed=7999118;
RA Konishi H., Shinomura T., Kuroda S.I., Ono Y., Kikkawa U.;
RT "Molecular cloning of rat RAC protein kinase alpha and beta and their
RT association with protein kinase C zeta.";
RL Biochem. Biophys. Res. Commun. 205:817-825(1994).
CC -I- FUNCTION: General protein kinase capable of phosphorylating
CC several known proteins.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic and nuclear after activation by
CC integrin-linked protein kinase 1 (ILK1) (By similarity).
CC -I- TISSUE SPECIFICITY: Widely expressed. Low levels found in liver
CC with slightly higher levels present in thymus and testis.
CC -I- DOMAIN: Binding of the ph domain to the phosphatidylinositol 3-
CC kinase alpha (PI(3)K) results in its targeting to the plasma
CC membrane.
CC -I- PTM: Phosphorylation on Thr-308 and Ser-473 is required for full
CC activity.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC RAC SUBFAMILY.
CC -I- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D30040; BAA06279.1; --
CC HSP; P05132; ICTP.
DR InterPro; IPR000719; Euk_pkinase.

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DR InterPro; IPR001849; PH.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR002290; Ser thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00433; pkinase C; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
KW DOMAIN 5 108 PH.
FT DOMAIN 150 408 PROTEIN KINASE.
FT NE_BIND 156 164 ATP (BY SIMILARITY).
FT BINDING 179 179 ATP (BY SIMILARITY).
FT ACT_SITE 274 274 BY SIMILARITY.
FT MOD_RES 308 308 PHOSPHORYLATION (BY PDPK1) (BY
FT SIMILARITY).
FT MOD_RES 473 473 PHOSPHORYLATION (BY ILK1) (BY
FT SIMILARITY).
SQ SEQUENCE 480 AA; 55735 MW; 5DCAAE7134366D04 CRC64;
Query Match 37.5%; Score 878; DB 1; Length 480;
Best Local Similarity 41.9%; Pred. No. 3.2e-54;
Matches 191; Conservative 81; Mismatches 146; Indels 38; Gaps 10;
Qy 18 RPR-----HKRAEAQKRSSES-----FLSLGAFMKQRMGLNDFIQK----- 55
Db 23 RPYFLKNDGTFTGYKERPDQVQRESPLNNSVAQCQLMKTERPRPNTFIIRCLQWTT 82
Qy 56 IANNSVACKRPE-----VQSLKISQDQPELMANNSPPP--SPSQINLGPSNP 105
Db 83 VIERTFHVTPEEREETWTAIQTVADGLKQEEETMDFRSGSPSDNSGAEEMEAVALAKPK 142
Qy 106 H-AKPSDFHFLKVIKSGFGKVLARHKAEEVAVKVLQKAILKKKEKHMSERNVL 164
Db 143 HRVTMNEFEYKLGKGTGKVLVKEKATGRYAMKILKEVIAKDEVAHTLITE-NRV 201
Qy 165 LKNVHFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCFLPRARYAAEIASAL 224
Db 202 LQNSRHPLTALKVYSQTHDRLCFVMEYANGGELFFHLRSRVSFSDRTREYGAIVSAL 261
Qy 225 GYLHS-LNIVYRDLPENILLDSQGHIVLTDPLCKENIEHNSITSTFCGTEYLAPVHL 283
Db 262 DYLSHSEKNNVYRDLPENILLDSQGHIVLTDPLCKENIEHNSITSTFCGTEYLAPVHL 321
Qy 284 HKQPDYRTVDWCLGAVLYEMLYGLPFPYSRNTAEMYNILNKPLQKNPNTNSARHLL 343
Db 322 ENDYGRADVDMGLGVVMEYMMCGRLPFPYNQDHEKLPFELLMEIRPPTLGSPEAKSL 381
Qy 344 GLLKQDRTKRL-GAKDDFMFEIKSHVFFSLINWDDLINKKITPPFNPVNSGPNDRHFDPE 402
Db 382 GLLKQDRTKRLGGSEDAKEIMQHRFFANIVMDVVEKLSPPFPKQVTSSETDTRYFDEE 441
Qy 403 FTEEPVNSIGKSPDSVLVTASVKEAAEAPLGSFYA 438
Db 442 FTAQMITITPPDQDDSMCEVDS--ERRPHFPQFSYS 475

RESULT 9
RAT_KLVAT
ID RAT_KLVAT STANDARD; PRT; 501 AA.
AC P31748;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE AKT kinase transforming protein (EC 2.7.1.-).
GN V-AKT.

```

```

OS AKT8 murine leukemia virus.
OC Viruses; Retroviral viruses; Retroviridae; Gammatetrovirus.
OX NCBI_TaxID=11790;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92022574; PubMed=1833819;
RA Bellacosa A., Testa J.R., Staal S.P., Teichlis P.N.;
RT "A retroviral oncogene, akt, encoding a serine-threonine kinase
  containing an SH2-like region.";
RL Science 254:274-277(1991).
CC -1- PFM: AUTOPHOSPHORYLATED ON THR AND SER RESIDUES.
CC -1- MISCELLANEOUS: THIS PROTEIN IS EXPRESSED AS A FUSED GAG-AKT
  POLYPROTEIN.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC RAC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -----
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CC -----
DR EMBL; M80675; AAA42545.1; --
DR PIR; B40831; KIMVT8.
DR HSP; P05132; ICTP.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR Oncogene; Transferase; Serine/threonine-protein kinase;
  Phosphorylation; ATP-binding.
FT DOMAIN 26 129
FT NP_BIND 171 429
FT BINDING 200 200
FT ACT_SITE 295 295
FT MOD_RES 347 347
FT SEQUENCE 501 AA; 57870 MW; 5AEFDE58CD42F773 CRC64;
Query Match 37.5%; Score 878; DB 1; Length 501;
Best Local Similarity 41.9%; Pred. No. 3.4e-54;
Matches 194; Conservative 77; Mismatches 140; Indels 52; Gaps 11;
Qy 18 RPR-----HKRAEAKRSES-----FLLSGLAFWKQRMGLNDFIQK----- 55
Db 44 RPRYFLKNDGTFIGYKERPDQVQDRESPLNFVSAQCQLMKTERPRENTFIIRCLQWTT 103
Qy 56 IANNYSACKHPE-----VQSLTKISQPEELMNAFPPSPS-----QQINLGPSS 103
Db 104 VIERTFHVEPEEREWEATATQTVDGLKQKEETMDFRSGSPSDNSGAEMEVSU----- 159
Qy 104 NPAKP-----SDFHLKVIKGSFGKLLARHAKBEVFYAVKVLQKAILKKKEKH 157
Db 160 ---AKPRHRTVMNEFEVLLKLGKTFGKVLVKEKATGRYAMKILKEVIAKDEVAHT 216
Qy 158 MSERNVLLKXVKKHFLVGLHFSFQADKLYFVLDYINGGELFYHLQRCFLEPRARFYA 217
Db 217 LTE-NRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGELFFLHRSRVFSEDRARFYG 275

RESULT 10
ID KRAC_MOUSE STANDARD; PRT; 480 AA.
AC P31750; Q62274;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE RAC-alpha serine/threonine kinase (EC 2.7.1.1-) (RAC-PK-alpha) (AKT1
  DE kinase) (Protein kinase B) (PKB) (C-AKT) (Thymoma viral proto-
  DE oncogene).
DE GN AKT1 OR AKT OR RAC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Bousquets X., Powell C.;
RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=AKR/J; TISSUE=Thymus;
RX MEDLINE=93173519; PubMed=8437858;
RA Bellacosa A., Franke T.F., Gonzalez-Portal M.E., Datta K., Taguchi T.,
RA Gardner J., Cheng J.Q., Testa J.R., Teichlis P.N.;
RT "Structure, expression and chromosomal mapping of c-akt: relationship
  RT to v-akt and its implications.";
RC Oncogene 8:745-754(1993).
CC -1- FUNCTION: General protein kinase capable of phosphorylating
  CC several known proteins.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear after activation by
  CC integrin-linked protein kinase 1 (ILK1) (By similarity).
CC -1- TISSUE SPECIFICITY: Widely expressed. Low levels found in liver
  CC with slightly higher levels present in thymus and testis.
CC -1- DOMAIN: Binding of the ph domain to the phosphatidylinositol 3-
  CC kinase alpha (PI(3)K) results in its targeting to the plasma
  CC membrane.
CC -1- PTM: Phosphorylation on Thr-308 and Ser-473 is required for full
  CC activity.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC RAC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -----
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CC -----
DR EMBL; M94335; AAA18254.1; --
DR EMBL; X65687; CAA46620.1; --
DR HSP; P05132; ICTP.
DR MGI; MGI:87986; Akt1.
DR InterPro; IPR000719; Euk_pkinase.

```


Db 292 ITDFGLSKK-IETDTGTFCTGPEYLAPEVLNGHGHGCAVDWMSLGLTLYEMLTGLPPF 350
 QY 312 YSRNTAEWYNILNKLQKPNITNSARHLLEGLOKDRKRLGAKDDFMEIKSHVPFSL 371
 Db 351 YQNVSTMYOKILNGELUKIPTYSPEAKSLLEGULTREVDRKLGKGG-GEVQKHPFKN 409
 QY 372 INWDLINKKITPPFNVSQPNLRFDFEFTPEEPVNSIGKSPDPSVLVTASVKEAA-- 429
 Db 410 IDMEKLORKEVVEHFVKPKVSGTDSIQDPVFTQE-----RPMDSLVETSALGDAMGK 462
 QY 430 -EAPLGFSAPTDSFL 445
 Db 463 DTSPEGTYV--ADSIL 477

RESULT 12

AKT2_HUMAN STANDARD; PRT; 481 AA.
 AC P31751;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RAC-beta serine/threonine protein kinase (EC 2.7.1.1-) (RAC-PK-beta)
 DE (Protein kinase Akt-2) (Protein kinase B, beta) (PKB beta).
 GN AKT2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Epithelium;
 RX MEDLINE=92198987; PubMed=1801921;
 RA Jones P.F., Jakubowicz T., Hemmings B.A.;
 RT "Molecular cloning of a second form of rac protein kinase.";
 RL Cell Regul. 2:1001-1009(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9302845; PubMed=1409633;
 RA Cheng J.Q., Godwin A.K., Bellacosa A., Taguchi T., Franke T.F.,
 RA Hamilton T.C., Tsichlis P.N., Testa J.R.;
 RT "AKT2, a putative oncogene encoding a member of a subfamily of
 RT protein-serine/threonine kinases, is amplified in human ovarian
 RT carcinomas.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:9267-9271(1992).
 CC -!- FUNCTION: GENERAL PROTEIN KINASE CAPABLE OF PHOSPHORYLATING
 CC SEVERAL KNOWN PROTEINS.
 CC -!- TISSUE SPECIFICITY: IN ALL HUMAN CELL TYPES SO FAR ANALYZED.
 CC -!- DISEASE: ALTERATIONS OF AKT2 MAY CONTRIBUTE TO THE PATHOGENESIS OF
 CC OVARIAN CARCINOMAS.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC RAC SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.

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 CC or send an email to license@ebi.ac.uk).

CC -----
 CC EMBL; M7198; AAA36585.1; -;
 CC ENBL; M95936; AAA58364.1; -;
 CC PIR; A46288; A46288.
 CC HSP; P05132; IAPM.
 CC Genew; HGNC:392; AKT2.
 CC MIM; 164731; -;
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR001849; PH.
 CC InterPro; IPR000961; Pkinase_C.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC Pfam; PF00069; pkinase; 1.

DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00433; pkinase C; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 KW transferase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 5 108 PH.
 FT DOMAIN 152 409 PROTEIN KINASE.
 FT NP_BIND 158 166 ATP (BY SIMILARITY).
 FT BINDING 181 181 ATP (BY SIMILARITY).
 FT ACT_SITE 275 275 BY SIMILARITY.
 FT CONFLICT 478 481 SIRE -> FREEKDLMSLVSVLILFSDFSLSKSHSFSSNF
 FT ILLSFSLKK (IN REF. 1).
 SQ SEQUENCE 481 AA; 55768 MW; B18C87A7246FB24 CRC64;
 Query Match 36.9%; Score 863.5; DB 1; Length 481;
 Best Local Similarity 42.6%; Pred. No. 3.3e-53;
 Matches 182; Conservative 70; Mismatches 138; Indels 37; Gaps 7;
 QY 18 RPR-----HKGAEAQKRS-----ESFLSLGLAFMKQRMGLNDFIOK----- 55
 Db 23 RPRFLLKSDSGFIGYKERPEAPDQTLPLNNSFVAECQLMKTERPRPNTFVIRCLQWTT 82
 QY 56 IANNSYACKHPE-----VQSILKISQEPPELMNANSPSPSPSQNLGPPSSN 104
 Db 83 VIERTFHVDSPDREEREMRAIOMVANSKQAPGEDPMYKCGSPSDSSTTEMEVAVSK 142
 QY 105 PHAK--PSPDFHLKVIKSGFGKGLARHKAEEVFYAVKVLQKAILKKKEEKHISERN 162
 Db 143 ARAKVTMNDFDYLLKLGKGTGKVLVREKATGRYAMKILRKEVLIADKDEVAHTVTESR 202
 QY 163 VLLKNVKKHPFLVGLHFSTQADKLYEVLVDYINGELFYHLQRCFLEPRARYAABIAS 222
 Db 203 V-LQNRHPFLTALKYAFQTHDLRCFVMEYANGELFFHLRSRVFTEERARYGAEIVS 261
 QY 223 ALGYLSLNIIVYRLDKPENILDSQGHIVLTDLGCKENIEHNSTSTPFCGTPEYLAPEV 282
 Db 262 ALEYLSRSDVYVYRDIKLENLMLDKGHIKITDGLCKEGISDGTATMKTFCGTPEYLAPEV 321
 QY 283 LHKQVPDRTVDWCLGAVLYEMLYGLPPFVSRNTAEWYNILNKLQKPNITNSARHLL 342
 Db 322 LEDNDYGRAVDWMLGVVMTYEMMCGRLPFYVQDHERLDFELIMEEIRFPRTLSPKAKSL 381
 QY 343 EGLLQKDRTKRL-GAKDDFMEIKSHVFFSLINWDDLINKKITPPFNVSQPNLRFDFP 401
 Db 382 AGLLKKDKPKORLGGSPDAKEVMEHFFLSINWQDVVQKLLPPFKPQVTSEVDTRYFDD 441
 QY 402 EFTPEPV 408
 Db 442 EFTAQSI 448

RESULT 13

KRAC_BOVIN STANDARD; PRT; 480 AA.
 ID KRAC_BOVIN
 AC Q01314;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE RAC-alpha serine/threonine kinase (EC 2.7.1.1-) (RAC-PK-alpha)
 DE (Protein kinase B) (PKB).
 GN AKT1 OR PKB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]


```
DR HSP; POS132; ICTP.
DR Genew; HGNC:391; AKT1.
DR MN; 164730; -.
DR InterPro; IPR001849; PH_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00169; PH; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S-TK_X; 1.
DR SMART; SM00220; S-TK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Nuclear protein.
FT DOMAIN 5 108
FT NP_BIND 150 408 PROTEIN KINASE.
FT BINDING 156 164 ATP (BY SIMILARITY).
FT BINDING 179 179 ATP (BY SIMILARITY).
FT ACT_SITE 274 274 BY SIMILARITY.
FT MOD_RES 308 308 PHOSPHORYLATION (BY PDPK1).
FT MOD_RES 473 473 PHOSPHORYLATION (BY ILK1).
FT MUTAGEN 308 308 T->D: 5-FOLD ACTIVATION, AND WHEN
ASSOCIATED WITH D-473; 18-FOLD
ACTIVATION.
FT MUTAGEN 473 473 S->D: 7-FOLD ACTIVATION, AND WHEN
ASSOCIATED WITH D-308; 25-FOLD
ACTIVATION.
FT CONFLICT 173 174 GR -> A (IN REF. 3).
FT CONFLICT 202 202 L -> Q (IN REF. 3).
FT CONFLICT 212 212 A -> R (IN REF. 3).
FT CONFLICT 246 246 S -> A (IN REF. 3).
FT CONFLICT 409 409 A -> T (IN REF. 3).
FT CONFLICT 476 476 A -> P (IN REF. 3).
FT CONFLICT 478 478 S -> A (IN REF. 3).
SQ SEQUENCE 480 AA; 55716 MW; 6EAF938AD436714 CRC64;

Query Match 36.8%; Score 861; DB 1; Length 480;
Best Local Similarity 42.3%; Pred. No. 4.9e-53;
Matches 189; Conservative 76; Mismatches 144; Indels 38; Gaps 10;

Qy 18 RPHKKAQAQKSEFLLSGLAEWQKORRMCLNDFIQK-----IANNYSACKHPE----- 67
Db 41 RPQVDQREAP--LNNFSVAQCQLMKTERPRPTFIIRCLQMTTIVERTFHVETPEERE 98
Qy 68 ----VQSILKISQPEPELMANPPSPSPS---QQINLGPSNPHAKP-----SDFH 113
Db 99 WTTAIVADGLKKQEEEMDFRSGSPSDNSGAEMEVS-----AKPKHRTVMNEFE 151
Qy 114 FLKVIKGSFGKVLARHKAEEVYAVKVLQKKAILKKKEKHIMSERNVLLKNVGHFFL 173
Db 152 YLKLLGKGTGKVLVREKATGRYAMKILKEVIVAKDEVAHTLSE-NRVLQNSRHFFL 210
Qy 174 VGLHFSQTADKLVFLDYINGGELFYHLQRCFLPRARFYAEIASALGYLHS-LNI 232
Db 211 TALKYSFQTHRLCFVMYANGGELFFHLSEVFSEDRARFYGAIEVSALDYLHSEKNV 270
Qy 233 VYRDLKPENILDSQGHIVLTDGCLCKENIEHNSTTFTCGTPEYLAPEVLHKQPYDRTV 292
Db 271 VYRDLKLENLMDKDGHIKITDFGLCKEGIKDGATMTFTCGTPEYLAPEVLEDNDYGRAV 330
Qy 293 DWKCLGAVLYEMLYGLPPFYSRNTAEYDNIILNKPQLQKNITNSARHLLGLELQKDRTK 352
Db 331 DWKGLGVVYEMMCGRLPPFYNDQHEKLFELILMEEIRPRTLGPGEAKSLLSGLLKKPKQ 390
Qy 353 RL-GAKDDFMEIKSHVFFSLINWDLLINKKITPPFNPNVSGPNDLRHDFDEFTPEEPVNS 411
Db 391 RLGGSSEDAKEIMQHRPFAGIVQHVYKELSPFPKQVTSMTDTTRYFDEEFTAQMITIT 450
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```
Qy 412 IGKSPDSVLVTASVKEAAEAFLGFSYA 438
|||
Db 451 PPQDDDSMECVDS--ERRPHFPQFSYS 475
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Search completed: June 20, 2003, 19:25:16
Job time : 25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:22:28 ; Search time 42 Seconds
(without alignments)
1018.567 Million cell updates/sec

Title: US-10-067-977-2
Perfect score: 2340
Sequence: 1 MGENQALARLESLLRPR.....KEAAEALGFSYAPPTDSFL 445
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2118	90.5	431	2	serum and glucocorticoid-regulated kinase - rat
2	1082	46.2	422	A48094	hypothetical prote
3	916	39.1	479	1	protein kinase C (
4	912	39.0	462	1	protein kinase C (
5	910	38.9	454	1	protein kinase C (
6	894	38.2	611	1	protein kinase C (
7	878	37.5	480	1	protein kinase C (
8	878	37.5	480	1	protein kinase C (
9	878	37.5	763	1	protein kinase C (
10	864.5	36.9	479	2	protein kinase C (
11	863.5	36.9	481	1	protein kinase C (
12	862	36.8	480	1	protein kinase C (
13	861	36.8	480	1	protein kinase C (
14	852.5	36.4	481	1	protein kinase C (
15	831.5	35.5	677	2	protein kinase C (
16	828	35.4	569	2	protein kinase C (
17	827.5	35.4	680	2	protein kinase C (
18	814	34.8	546	1	protein kinase C (
19	812	34.7	481	2	protein kinase C (
20	807	34.5	525	1	protein kinase C (
21	807	34.5	525	1	protein kinase C (
22	801.5	34.3	541	1	protein kinase C (
23	799	34.1	634	1	protein kinase C (
24	798	34.1	525	1	protein kinase C (
25	796.5	34.0	1016	1	protein kinase C (
26	791.5	33.8	672	1	protein kinase C (
27	791.5	33.8	672	1	protein kinase C (
28	791.5	33.8	672	1	protein kinase C (
29	790.5	33.8	672	1	protein kinase C (

ALIGNMENTS

RESULT 1

A48094
serum and glucocorticoid-regulated kinase - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 19-Dec-1997
C:Accession: A48094
R:Webster, M.K.; Goya, L.; Ge, Y.; Maiyar, A.C.; Firestone, G.L.
Mol. Cell. Biol. 13, 2031-2040, 1993
A:Title: Characterization of sgk, a novel member of the serine/threonine protein kinase
A:Reference number: A48094; MUID:93204949; PMID:8455596
A:Accession: A48094
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-431 <WEB>
A:Experimental source: Con8.hdc mammary epithelial tumor cells
A:Note: sequence extracted from NCBI backbone (NCBIN:127618, NCBIPI:127619)
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
C:Keywords: ATP
F:96-355/Domain: protein kinase homology <KIN>
F:104-112/Region: protein kinase ATP-binding motif

Query Match	90.5%	Score 2118;	DB 2;	Length 431;
Best Local Similarity	97.3%	Pred. No. 1.5e-87;		
Matches	396;	Conservative	7;	Mismatches 4; Indels 0; Gaps 0;
Qy	39	LAFWKQRMGLNDFIQKIANNYSACKHPEVQSILKISQPEPELMNANPPSPSPSQOIN	98	
Db	25	IAPFKQRMGLNDFIQKIANNYSACKHPEVQSILKISQPEPELMNANPPSPSPSQOIN	84	
Qy	99	LGSSNPXAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKLVQKAILKKKEKHIM	158	
Db	85	LGSSNPXAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKLVQKAILKKKEKHIM	144	
Qy	159	SERNVLKNNKHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRECFLEPRARYAA	218	
Db	145	SERNVLKNNKHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRECFLEPRARYAA	204	
Qy	219	EIASALGYLHSLNIVYRDLKPENILDSQGHIVLTFGLCKENIEHNSTSTPCTGTEYL	278	
Db	205	EIASALGYLHSLNIVYRDLKPENILDSQGHIVLTFGLCKENIEHNSTSTPCTGTEYL	264	
Qy	279	APVHLKQPDVDRVDMWCLGAVLYEMLYGLPPFSRNTAEVYNILNKPLQKPNITNSA	338	
Db	265	APVHLKQPDVDRVDMWCLGAVLYEMLYGLPPFSRNTAEVYNILNKPLQKPNITNSA	324	
Qy	339	RHLEGLLQKDRTKRLGAKDDFMKISHVFFSLINWDDLKINKITPPFNPNVSGPNDLRH	398	
Db	325	RHLEGLLQKDRTKRLGAKDDFMKISHVFFSLINWDDLKINKITPPFNPNVSGPNDLRH	384	
Qy	399	FDPEFTEEPVNPISGKSPDSVLVTASVKEAAEALGFSYAPPTDSFL	445	
Db	385	FDPEFTEEPVNPISGKSPDSVLVTASVKEAAEALGFSYAPPTDSFL	431	

A;Residues: 1-462 <POU>
A;Cross-references: EMBL:AL117525; GB: CAB55977; NID: G5912043; PIDN: CAB55977.1
A;Experimental source: adult testis; clone DKFp434N0250
R; Nakatani, K.; Thompson, D.A.; Barthel, A.; Sakau, H.; Liu, W.; Weigel, R.J.; Roth, R.
J. Biol. Chem. 274, 21528-21532, 1999
A;Title: Up-regulation of Akt3 in estrogen receptor-deficient breast cancers and androgen
A;Reference number: A64199; PMID: 10419456
A;Comments: annotation
A;Comment: This protein is increased in estrogen receptor-negative breast cancers and an
C;Genetics:
A;Gene: GDB:AKT3
A;Cross-references: GDB:9954867
A;Map position: 1q44-1q44
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F;4-105/Domain: pleckstrin repeat homology <PLK>
F;146-405/Domain: protein kinase homology <PK>
F;154-162/Region: protein kinase ATP-binding motif
F;177/Active site: Lys #status predicted

Query Match 39.08; Score 912; DB 1; Length 462;
Best Local Similarity 47.08; Pred. No. 5.1e-34;
Matches 187; Conservative 63; Mismatches 120; Indels 28; Gaps 7;
QY 33 SFLSLGLAFMKQRMGLNDFIQK-----IANNYSACKHPE-----VQSILKISQPO 78
DB 53 NFSVAKCOLMKTTERPKNTFIIRCLQWTTVIERTFHVDTPEEREWEATEIQAVADRLQ 112
QY 79 EPELMANPPSPSPSQOINLG-----PSSNPHAK-----PSDFHLKLVIGKSGFGKVLARH 131
DB 113 EERMNCSPT-----SQIDNIGEEEMDASTTHHKRTMNDFDYLLKLGKTFGKVLVRE 167
QY 132 KAEVEFYAVKVLQKAILKKKEKHIMSRNVLKNVHFLVGLHFSFQTADKLFLVLD 191
DB 168 KASGKYAMKILKEVIIIAKDEVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVME 226
QY 192 YINGGELFYHLQERCFLEPRARFYAAEIASALGYLHSLNIVYRDLPENILDSQGHV 251
DB 227 YNGGELFFHLSERVSEDRTRFYGAIEVSALDYLSHGKIVYRDLPENILDSQGHV 286
QY 252 LTDFGLCKENIEHNSTTSCGTPPEYLAPEVLHKKQPYDRTVDMWCLGAVLYEMLYGLPPF 311
DB 287 ITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLHKKQPYDRTVDMWCLGAVLYEMLYGLPPF 346
QY 312 YSRNTAEWYDNLINKPQLKPNITNSARHLEGLLOKDRKRL-GAKDDFMEIKSHVFFS 370
DB 347 YNQDHEKFLILMEDIKFPTLSSDAKSLSLGLLKDPNKRLGGGPDPAKEIMRHSFFS 406
QY 371 LINWDDLKINKITPPPNPNVSGNDLRFHDPETEPV 408
DB 407 GVNWQDVYDKLVPPPKPQVTSYDTRFDEEFTAQTI 444

RESULT 5
JC4345
protein kinase (EC 2.7.1.37) akt3 [validated] - rat
N;Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
C;Accession: JC4345
R;Konishi, H.; Kuroda, S.; Tanaka, M.; Matuzaki, H.; Ono, Y.; Kameyama, K.; Haga, T.; K
Biochem. Biophys. Res. Commun. 216, 526-534, 1995
A;Title: Molecular cloning and characterization of a new member of the RAC protein kinase
e C subtypes and beta gamma subunits of G proteins.
A;Reference number: JC4345; PMID: 96063640; PMID: 7488143
A;Accession: JC4345
A;Molecule type: mRNA
A;Residues: 1-454 <KON>
A;Cross-references: DDBJ:D49836; NID: g1136777; PIDN: BAA08637.1; PID: g1401040
A;Experimental source: brain

C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein
F;4-105/Domain: pleckstrin repeat homology <PLK>
F;146-405/Domain: protein kinase homology <PK>
F;154-162/Region: protein kinase ATP-binding motif
F;177/Active site: Lys #status predicted

Query Match 38.9%; Score 910; DB 1; Length 454;
Best Local Similarity 47.0%; Pred. No. 6.1e-34;
Matches 187; Conservative 63; Mismatches 120; Indels 28; Gaps 7;
QY 33 SFLSLGLAFMKQRMGLNDFIQK-----IANNYSACKHPE-----VQSILKISQPO 78
DB 53 NFSVAKCOLMKTTERPKNTFIIRCLQWTTVIERTFHVDTPEEREWEATEIQAVADRLQ 112
QY 79 EPELMANPPSPSPSQOINLG-----PSSNPHAK-----PSDFHLKLVIGKSGFGKVLARH 131
DB 113 EERMNCSPT-----SQIDNIGEEEMDASTTHHKRTMNDFDYLLKLGKTFGKVLVRE 167
QY 132 KAEVEFYAVKVLQKAILKKKEKHIMSRNVLKNVHFLVGLHFSFQTADKLFLVLD 191
DB 168 KASGKYAMKILKEVIIIAKDEVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVME 226
QY 192 YINGGELFYHLQERCFLEPRARFYAAEIASALGYLHSLNIVYRDLPENILDSQGHV 251
DB 227 YNGGELFFHLSERVSEDRTRFYGAIEVSALDYLSHGKIVYRDLPENILDSQGHV 286
QY 252 LTDFGLCKENIEHNSTTSCGTPPEYLAPEVLHKKQPYDRTVDMWCLGAVLYEMLYGLPPF 311
DB 287 ITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLHKKQPYDRTVDMWCLGAVLYEMLYGLPPF 346
QY 312 YSRNTAEWYDNLINKPQLKPNITNSARHLEGLLOKDRKRL-GAKDDFMEIKSHVFFS 370
DB 347 YNQDHEKFLILMEDIKFPTLSSDAKSLSLGLLKDPNKRLGGGPDPAKEIMRHSFFS 406
QY 371 LINWDDLKINKITPPPNPNVSGNDLRFHDPETEPV 408
DB 407 GVNWQDVYDKLVPPPKPQVTSYDTRFDEEFTAQTI 444

RESULT 6
A55888
protein kinase (EC 2.7.1.37) akt [similarity] - fruit fly (Drosophila melanogaster)
N;Alternate names: protein kinase B; RAC-PK; serine/threonine-specific protein kinase R
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2001
C;Accession: A55888
R;Andjelkovic, M.; Jones, P.F.; Grossniklaus, U.; Cron, P.; Schier, A.F.; Dick, M.; Bil
J. Biol. Chem. 270, 4066-4075, 1995
A;Title: Developmental regulation of expression and activity of multiple forms of the D
A;Reference number: A55888; MUID: 95181376; PMID: 7876156
A;Accession: A55888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-611 <AND>
A;Cross-references: GB: X83510
C;Genetics:
A;Gene: FlyBase: RacPK
A;Cross-references: FlyBase: Fggn0013324
A;Start codon: ACG
A;Introns: 261/3; 327/3; 457/3; 535/3; 584/3
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphorotransferase; phosphotransferase; serine/threon
F;105-209/Domain: pleckstrin repeat homology <PLK>
F;264-523/Domain: protein kinase homology <PK>
F;272-280/Region: protein kinase ATP-binding motif
F;295/Active site: Lys #status predicted

F;423/Binding site: phosphate (Thr) (covalent) #status predicted
F;566/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 38.2%; Score 894; DB 1; Length 611;
Best Local Similarity 54.3%; Pred. No. 4.1e-33;
Matches 178; Conservative 45; Mismatches 99; Indels 6; Gaps 4;

QY 111 DFHFLKVIKSGSGKVLARHKAEEVFYAVKVLQKAILKKKEKHMSERNVLLKNVXH 170
DB 265 NFBEFLKVLGKGTGKVLCKREKATAKAIKILKEVILQKDEVAHFTLTESRV-LKSTNH 323
QY 171 PFVLGLHFSQTDADKLVFLVDYINGGELFYHLQRCFLPRARFYAAEIASALGYLHSL 230
DB 324 PFLISLKYSTQNDRLCFVQYNGGELFWHLSHERIFTEDRTFYGAEEIISALGYLHSG 383
QY 231 NIVYRDLKPNILDSOGHIVLDFGLCKENIEHNSTSTFCGTPPEYLADEVHLKQPYDR 290
DB 384 GIIYRDLKLENLLDKDGHIKVADFGLEKEDITYGRTTKTCGTPPEYLADEVLLDNDYQG 443
QY 291 TVDWMLGAVLYEMLYGLPFYSRNTAEMVDNLKPLQKPNITNSARHLLGGLQKOR 350
DB 444 AVDMWGTGVVYEMICGRLPFYNDHDVLFLLILVEEVKFRNITDEAKNLLAGLLAKOP 503
QY 351 TKRL-GAKDDFMELIKSHVFFSLNWDLLINKKITPPENPNVSGPNDLRFDPFTPEPVP 409
DB 504 KRLGGGKDDVKEIQAHFFASINWTDVLKTKPPPPKQVTSDDTRFYDKFTGESVE 563
QY 410 NSIGKSPDSVLVTASVKEAAEAFIGFSY 437
DB 564 LT---PPDPTGPLGSIAE-EPLFPQFSY 587

RESULT 7

JC2437
protein kinase (EC 2.7.1.37) akt1 [validated] - rat
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 20-Apr-2001
C;Accession: JC2437

R;Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.
Biochem. Biophys. Res. Commun. 205, 817-825, 1994
A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their associati
A;Reference number: JC2437; MUID:95091823; PMID:7999118
A;Accession: JC2437
A;Molecule type: mRNA
A;Residues: 1-480 <KON>
A;Cross-references: DDBJ:D30040; NID:9485402; PIDN:BA06279.1; PID:9485403
A;Experimental source: testis
C;Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;148-408/Domain: protein kinase homology <KIN>
F;156-164/Region: protein kinase ATP-binding motif
F;179/Active site: Lys #status predicted
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte

Query Match 37.5%; Score 878; DB 1; Length 480;
Best Local Similarity 41.9%; Pred. No. 1.7e-32;
Matches 191; Conservative 81; Mismatches 146; Indels 38; Gaps 10;

QY 18 RPR-----HKRAEAKRSES-----FLLSGLAFMKQRMGLNDFIQK----- 55
DB 23 RPRYFLKNDGDTFTGYKERPDVQRESPLNFSVAQCQLMKTERPRPNTFIIRCLQWTT 82
QY 56 IANNSYACKHPE-----VQSILKISQPEPELMNANSPPP--SPSQOINLGPSNP 105
DB 83 VIERTFVETPEEREWTATITQTVADGLKQKEETMDFRSGSPSDNSGAEEMEVAKPK 142
QY 106 H-AKPSDFHFLKVIKSGSGKVLARHKAEEVFYAVKVLQKAILKKKEKHMSERNVL 164

DB 143 HRVTWNEFEYKLGKGTGKVLVKEKATGRYAMKILKKEIVAKDEVAHFTLTSE-NRV 201
QY 165 LKNVGHFPFLVGLHFSQTDADKLVFLVDYINGGELFYHLQRCFLPRARFYAAEIASAL 224
DB 202 LQNSRHPFLTALKYSQTDHRLCFVMEYANGGELFFHLSSRERFVSSDRARFYGAETVSAL 261
QY 225 GYLHS-LNIVYRDLKPNILDSOGHIVLDFGLCKENIEHNSTSTFCGTPPEYLADEVL 283
DB 262 DYLHSEKNVYVYRDLKLENLLDKDGHIKITDFGLCKEGIKDGNATMTFCGTPPEYLADEVL 321
QY 284 HKQPYDRTYDWMLGAVLYEMLYGLPFYSRNTAEMVDNLKPLQKPNITNSARHLL 343
DB 322 EDNDYGRAVDWMLGAVLYEMLYGLPFYSRNTAEMVDNLKPLQKPNITNSARHLL 381
QY 344 GLLQKQRTKRL-GAKDDFMELIKSHVFFSLNWDLLINKKITPPENPNVSGPNDLRFDP 402
DB 382 GLLKKDPTQRLGGSGSDAKEIMQHRFFANIVMDVYEKLSPPFPKQVTSDDTRFYD 441
QY 403 FTEEPVPNSIGKSPDSVLVTASVKEAAEAFIGFSY 438
DB 442 FTAQMIIITPPDQDDSMECVDS--ERRPHFPQFSYS 475

RESULT 8

S33364

protein kinase (EC 2.7.1.37) akt1 [similarity] - mouse
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prot
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2001
C;Accession: S33364
R;Bellacosa, A.; Franke, T.F.; Gonzalez-Portal, M.E.; Datta, K.; Taguchi, T.; Gardner,
Oncogene 8, 745-754, 1993
A;Title: Structure, expression and chromosomal mapping of c-akt: relationship to v-akt
A;Reference number: S33364; MUID:93173519; PMID:8437858
A;Accession: S33364
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-480 <BEL>
A;Cross-references: EMBL:X65687; NID:9287806; PIDN:CAA46620.1; PID:9287807
C;Genetics:

A;Gene: MGI:Akt
A;Cross-references: MGI:87986
A;Map position: 12
C;Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-throni
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;148-408/Domain: protein kinase homology <KIN>
F;156-164/Region: protein kinase ATP-binding motif
F;179/Active site: Lys #status predicted
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein k
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict

Query Match 37.5%; Score 878; DB 1; Length 480;
Best Local Similarity 41.9%; Pred. No. 1.7e-32;
Matches 194; Conservative 77; Mismatches 140; Indels 52; Gaps 11;

QY 18 RPR-----HKRAEAKRSES-----FLLSGLAFMKQRMGLNDFIQK----- 55
DB 23 RPRYFLKNDGDTFTGYKERPDVQRESPLNFSVAQCQLMKTERPRPNTFIIRCLQWTT 82
QY 56 IANNSYACKHPE-----VQSILKISQPEPELMNANSPPPSPS-----QQINLGPS 103
DB 83 VIERTFVETPEEREWEATAIQTVADGLKQKEETMDFRSGSPSDNSGAEEMEVSL----- 138
QY 104 NPAKPE-----SDFHFLKVIKSGSGKVLARHKAEEVFYAVKVLQKAILKKKEKH 157
DB 139 ---AKPRHVTWNEFEYKLGKGTGKVLVKEKATGRYAMKILKKEIVAKDEVAHFT 195
QY 158 MSERNVLLKNVGHFPFLVGLHFSQTDADKLVFLVDYINGGELFYHLQRCFLPRARFYA 217

N;Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein kinase
 C;Species: Homo sapiens (man)
 C;Date: 22-Sep-1993 #sequence_revision 12-May-1994 #text_change 31-Mar-2001
 C;Accession: A46288
 R;Cheng, J.Q.; Godwin, A.K.; Bellacosa, A.; Taguchi, T.; Franke, T.F.; Hamilton, T.C.; et al. Proc. Natl. Acad. Sci. U.S.A. 89, 9267-9271, 1992
 A;Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-serine/threonine kinases
 A;Reference number: A46288; MUID:93028445; PMID:1409633
 A;Accession: A46288
 A;Molecule type: mRNA
 A;Residues: 1-481 <CHE>
 A;Cross-references: GB:M95936; NID:G178325; PIDN:AAA58364.1; PID:G178326
 A;Note: sequence extracted from NCBI backbone (NCBIP:115959)
 C;Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas.
 C;Genetics:
 A;Gene: GDB:AKT2
 A;Cross-references: GDB:135660; OMIM:164731
 A;Map position: 19q13.2-19q13.2
 C;Function:
 A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
 A;Pathway: signal transduction pathways regulating various processes
 C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
 C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
 F;4-106/Domain: pleckstrin repeat homology <PLK>
 F;150-409/Domain: protein kinase homology <KIN>
 F;158-166/Region: protein kinase ATP-binding motif
 F;181/Active site: Lys #status predicted

Query Match 36.9%; Score 863.5; DB 1; Length 481;
 Best Local Similarity 42.6%; Pred. No. 7.4e-32;
 Matches 182; Conservative 70; Mismatches 138; Indels 37; Gaps 7;

QY 18 RPR-----HKRAEAQKRS-----ESFLSGLAFPMKQRRMGLNDFIOK----- 55
 DB 23 RPRYFLKDGSGFTGYKERPEADQTLPLNFSVAECQLMKTERPRNPTFVIRCLQWTT 82
 QY 56 IANNSVACKHPE-----VOSILKISQPELNMNANPSPSPSQQINLGPSN 104
 DB 83 VIERTFHVDSFDEREEMRAIQVANSKQRAQGEDPMYDKCGSPSDSTTEMEVAVSK 142
 QY 105 PHAK--PSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEKHMSERN 162
 DB 143 ARAKVTMNDPYLLKLGKTFGKVLVREKATGRYAMKILRKEVIIAKDEVAHTVESR 202
 QY 163 VLLKNVCHPELVGLHFSFQADKLYFVLDYINGGELFYHLORERCFLEPPARFYAAEIAS 222
 DB 203 V-LQNRHFLTALKYAFQTHDRLCFVMEYANGELFFHLRSRERVFTEERARFYGABIVS 261
 QY 223 ALGYLHSLNTVYRDLKPEINLLDSQGHIVLTFGLCKENIEHNSTSTFCGTPEYLAPEV 282
 DB 262 ALGYLHSLNTVYRDLKPEINLLDSQGHIVLTFGLCKENIEHNSTSTFCGTPEYLAPEV 321
 QY 283 LHKQPYDRTYDVMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLKKNITNSARHLL 342
 DB 322 LEDNDYGRAVDWMLGVVYEMMCGRLFFYNQDHERLFELILMEIRFRTLSPEAKSL 381
 QY 343 EGLLOKDRTEL--CAKDDFMEIKSHVFFSLINWDDLLINKKITPPFNPNVSGPNDLRHFD 401
 DB 382 AGLLKDKPKQKRGGSDEAKVEHREHFLFSINWQVVOVKLLPPFKPQVTSVDTRYFDD 441
 QY 402 EFTPEEV 408
 DB 442 EFTAQSI 448

RESULT 12
 S62117
 protein kinase (EC 2.7.1.37) akt1 [similarity] - bovine
 N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protein kinase
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 14-Dec-2001
 C;Accession: S62117; S24423; S17999; S15714; S36388
 R;Coffer, P.J.; Woodgett, J.R.

submitted to the EMBL Data Library, December 1991
 A;Reference number: S62117
 A;Accession: S62117
 A;Molecule type: mRNA
 A;Residues: 1-480 <COF>
 A;Cross-references: EMBL:X61036; NID:G630; PIDN:CAA43371.1; PID:G631
 A;Note: this is a revision to the sequence from reference S17999
 R;Coffer, P.J.; Woodgett, J.R.
 Eur. J. Biochem. 205, 1217, 1992
 A;Reference number: S24423; MUID:92249329; PMID:1533586
 A;Contents: erratum
 A;Accession: S24423
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 70-78, N', 80-145 <COV>
 A;Cross-references: EMBL:X61036
 A;Note: this is a revision to the sequence from reference S17999
 R;Coffer, P.J.; Woodgett, J.R.
 Eur. J. Biochem. 201, 475-481, 1991
 A;Title: Molecular cloning and characterisation of a novel putative protein-serine kinase
 A;Reference number: S17999; MUID:92037600; PMID:1718748
 A;Accession: S17999
 A;Molecule type: mRNA
 A;Residues: 1-70, 'TPSSAAACGPRSSARSSTWRPRSGVDHRRPDGGRRAQAGGDDGLFVGLTRRELGGRGDGVAGV
 A;Cross-references: EMBL:X61036
 A;Note: this sequence has been revised in references S62117 and S24423
 C;Function:
 A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
 A;Pathway: signal transduction pathways regulating various processes
 C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
 C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen
 F;4-106/Domain: pleckstrin repeat homology <PLK>
 F;148-408/Domain: protein kinase homology <KIN>
 F;156-164/Region: protein kinase ATP-binding motif
 F;179/Active site: Lys #status predicted
 F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein k
 F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict

Query Match 36.8%; Score 862; DB 1; Length 480;
 Best Local Similarity 41.0%; Pred. No. 8.6e-32;
 Matches 190; Conservative 80; Mismatches 141; Indels 52; Gaps 11;

QY 18 RPR-----HKRAEAQKRS-----FLLSGLAFPMKQRRMGLNDFIOK----- 55
 DB 23 RPRYFLKNDGTFGYKERPDLEQRESPLNFSVAQCQLMKTERPRNPTFIRCLQWTT 82
 QY 56 IANNSVACKHPE-----VOSILKISQPELNMNANPSPSPSPS---QQINLGPS 103
 DB 83 VIERTFHVTEPEREEMTTAQTVDGLKQREBETMDFRSGSPGNSGABEMEVS--- 138
 QY 104 NPAKP-----SDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEKHI 157
 DB 139 ---AKPKHRVTWNEFVYKLLGKTFGKVLVKEKATAAYYAMKILKEVIVAKDEVAHT 195
 QY 158 MSERNVLLKNVCHPELVGLHFSFQADKLYFVLDYINGGELFYHLORERCFLEPPARFYA 217
 DB 196 LTF-NRVLQNSRHPSTALKYSFQTHDRLCFVMEYANGELFFHLRSRERVFSEDRARFY 254
 QY 218 AETASALGYLHS--LNTVYRDLKPEINLLDSQGHIVLTFGLCKENIEHNSTSTFCGTPE 276
 DB 255 AEIVSALDYHSEKEVYVRDLKLENLMDKDGHIKITDFGLCKEGIKDGMATMTKTCGTPE 314
 QY 277 YLAPEVLHKQPYDRTYDVMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLKKNITN 336
 DB 315 YLAPEVLEDNDYGRAVDWMLGVVYEMMCGRLFFYNQDHEKLFELILMEIRFRTLS 374
 QY 337 SARHLEGLLOKDRTEL--CAKDDFMEIKSHVFFSLINWDDLLINKKITPPFNPNVSGPND 395
 DB 375 EAKSLSGLLKKDKPKQKRGGSDEAKVEIMQHRFASIVQDVYKELKSLSPFPKQVTS 434
 QY 396 LRHFDPEFTPEEPVNSIGKSPSVLVTASVKEAAEAFLOFSYA 438
 DB 435 TRYFDEEFTAQMITITPPQDDDSMEGVDS--ERRPHFPQPSYS 475

RESULT 13

A39360
 protein kinase (EC 2.7.1.37) akt1 [validated] - human
 N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protein kinase
 C;Species: Homo sapiens (man)
 C;Date: 20-Mar-1992 #sequence_revision 12-May-1994 #text_change 30-Sep-2001
 C;Accession: A39360; S36389; S18000; S20836
 R;Jones, P.F.; Jakubowicz, T.; Picossi, F.J.; Maurer, F.; Hemmings, B.A.
 Proc. Natl. Acad. Sci. U.S.A. 88, 4171-4175, 1991
 A;Title: Molecular cloning and identification of a serine/threonine protein kinase of the human T cell leukemia virus type I tax gene
 A;Reference number: A39360; MUID:91239529; PMID:1851997
 A;Accession: A39360
 A;Molecule type: mRNA
 A;Residues: 1-480 <JON>
 A;Cross-references: GB:M63167; NID:G190827; PIDN:AAA36539.1; PID:G190828
 R;Coffer, P.J.; Woodgett, J.R.
 Eur. J. Biochem. 205, 1217, 1992
 A;Reference number: S24423; MUID:92249329; PMID:1533586
 A;Contents: extratum
 A;Accession: S36389
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: mRNA
 A;Residues: 63-172, 'A', 175-201, 'Q', 203-211, 'R', 213-245, 'A', 247-408, 'T', 410-475, 'P', 477, 'P', 480-480
 A;Cross-references: EMBL:X61037; NID:G35480; PIDN:CAA43372.1; PID:G35481
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1991
 A;Note: this is a revision to the sequence from reference S17999
 R;Coffer, P.J.; Woodgett, J.R.
 Eur. J. Biochem. 201, 475-481, 1991
 A;Title: Molecular cloning and characterisation of a novel putative protein-serine kinase
 A;Reference number: S17999; MUID:92037600; PMID:1718748
 A;Accession: S18000
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 63-70, 'TPSSNAACGGPLSSNAPSWRLRSGGVNRRHPCGRRPQ', 'EAGGGDGLPVLGTORQLRGRDRGGV'
 A;Cross-references: EMBL:X61037
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991
 A;Note: this sequence has been revised in reference S24423
 R;Coffer, P.
 submitted to the EMBL Data Library, July 1991
 A;Reference number: S20836
 A;Accession: S20836
 A;Molecule type: mRNA
 A;Residues: 63-70, 'TPSSNAACGGPLSSNAPSWRLRSGGVNRRHPCGRRPQ', 'EAGGGDGLPVLGTORQLRGRDRGGV'
 A;Cross-references: EMBL:X61037
 A;Note: this sequence has been revised in reference S24423
 R;Alessi, D.R.; Andjelkovic, M.; Caudwell, B.; Morrice, N.; Cohen, P.; Hemming, B.A.
 EMBO J. 15, 6341-6551, 1996
 A;Title: Mechanism of activation of protein kinase B by insulin and IGF-1.
 A;Reference number: A64192; MUID:97133284; PMID:8978681
 A;Contents: annotation; phosphorylation sites
 R;Toker, A.; Newton, A.C.
 J. Biol. Chem. 275, 8271-8274, 2000
 A;Title: Akt/protein kinase B is regulated by autophosphorylation at the hypothetical phosphorylation site
 A;Reference number: A64193; MUID:20187529; PMID:10722653
 A;Contents: annotation; autophosphorylation site
 C;Comment: Akt1 is ubiquitous as an inactive multimeric complex. It binds phosphatidylinositol (3-OH)phosphate and becomes fully active.
 C;Genetics:
 A;Gene: GDB:AKT1; RAC; PKB
 A;Cross-references: GDB:118989; OMIM:164730
 A;Map position: 14q32.32-14q32.32
 C;Function:
 A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate
 A;Pathway: signal transduction pathways regulating various processes including insulin resistance
 C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
 C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
 F;4-106/Domain: pleckstrin repeat homology <PLK>
 F;148-408/Domain: protein kinase homology <KIN>
 F;156-164/Region: protein kinase ATP-binding motif
 F;179/Active site: Lys #status predicted

F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein kinase)
 F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status experiment
 Query Match 36.8%; Score 861; DB 1; Length 480;
 Best Local Similarity 42.3%; Pred. No. 9.6e-12;
 Matches 189; Conservative 76; Mismatches 144; Indels 38; Gaps 10;
 QY 18 RPRHKRAEAQKRESFLLSGLAFMKORRMGLNDFIQK-----IANNYSACKHPE---- 67
 DB 41 RPQVDQREAP--LNNFVAQCQLMKTERRPRPNTFIIRCLQWTVIERTFVETPEEREE 98
 QY 68 ----VQSILKISQPOPELMNANPPSPSPS-----QQINLGPSNPHAKP-----SDPH 113
 DB 99 WTTAIQTQVADGLKKQBEEMDFRSGSPSDNSGAEMEVSLSL-----AKPKHRVTWNEFE 151
 QY 114 FLKVIKGSFGKVLARHKAEEVYAVKVLQKAILKKKEKHIMSGERNVLLKNVHPFL 173
 DB 152 YLKLLKGTGFKVILVKEKATGRYAMKILKKEVIVAKDEVAVTLTE--NRVLQNSRHPFL 210
 QY 174 VGLHFSQFQTADKLYFYLDYINGGELFYHLQRCFLPRARFYAAEIASALGYLHS--LNI 232
 DB 211 TALKYSFQTHDRLCFVMEYANGGELFFHLRSRVFSEDRAFYGAIEVSALDYLHSEKNV 270
 QY 233 VYRDLKPEINLLDSQGHIVLTDFGLCKENIEHNSSTSTFCGTPCYLAPEVLHKQPYDRTV 292
 DB 271 VYRDLKLENLMDKDGHIKITDFGLCKEGIKDGTATMKTFCGTPCYLAPEVLEDNDYGRAV 330
 QY 293 DMWCLGAVLYEMLYGLPPFVSRVTAEMYNILNKLQKPNITNSARHLLGGLQKDRTK 352
 DB 331 DMWGLGVMYEMMCGRLPFYNQDHEKLFEILMEEIRFPRTLGPKEAKSLUGLLKKDPKQ 390
 QY 353 RL-GAKDDFMEIKSHVFFSLINWDDLLINKITPPFNPVNSGPNDRHDFEFTEEPVPNS 411
 DB 391 RLGGSGSEDAKEINQHRFFAGIVQHVVEKLSPPFKPQVTSSETDTRFYDEEFTAQMITIT 450
 QY 412 IGKSPDSVLVTASVKAAEAFLGFSVA 438
 DB 451 PPQDDSDMECVDS--ERRPHFPQFSYS 475
 RESULT 14
 JC2438
 protein kinase (SC 2.7.1.37) akt2 [validated] - rat
 N;Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein kinase
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
 C;Accession: JC2438
 R;Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.
 Biochem. Biophys. Res. Commun. 205, 817-825, 1994
 A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their association with phosphoinositide 3-kinase
 A;Reference number: JC2437; MUID:95091823; PMID:7999118
 A;Accession: JC2438
 A;Molecule type: mRNA
 A;Residues: 1-481 <KON>
 A;Cross-references: DDBJ:D330041; NID:G485404; PIDN:BAA06280.1; PID:G485405
 A;Experimental source: testis
 C;Function:
 A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate
 A;Pathway: signal transduction pathways regulating various processes including myoblast differentiation
 C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
 C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
 F;4-106/Domain: pleckstrin repeat homology <PLK>
 F;150-409/Domain: protein kinase homology <KIN>
 F;158-166/Region: protein kinase ATP-binding motif
 F;181/Active site: Lys #status predicted
 Query Match 36.4%; Score 852.5; DB 1; Length 481;
 Best Local Similarity 42.2%; Pred. No. 2.3e-31;
 Matches 180; Conservative 71; Mismatches 139; Indels 37; Gaps 7;
 QY 18 RPR-----HKKRAEAQKRS-----ESFLSGLAFMKORRMGLNDFIQK----- 55
 DB 23 RPRYFLKSDGSGFIGYKERPEAPDOTLPPLNNFSAECQLMKTERPRNPTFVIRCLQWTT 82

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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:26:53 ; Search time 51 Seconds
(without alignments)
944.157 Million cell updates/sec

Title: US-10-067-977-2

Perfect score: 2340

Sequence: 1 MGEMOALARARLESLLRPR.....KEAAEAFLGFSVAPPTDSFL 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA*

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14: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2154	92.1	431	9	US-09-981-353-7
2	2150	91.9	431	9	US-10-000-039-2
3	2146	91.7	431	10	US-09-810-808-5
4	2100.5	89.8	430	10	US-09-810-808-9
5	1481	63.3	496	10	US-09-784-249-2
6	1411	60.3	367	10	US-09-971-118-2
7	968.5	41.4	276	9	US-09-764-868-669
8	916	39.1	479	10	US-09-771-161A-246
9	916	39.1	479	10	US-09-771-161A-247
10	916	39.1	479	10	US-09-771-161A-248
11	912	39.0	455	9	US-09-526-043-2
12	910	38.9	454	9	US-09-526-043-17
13	889	38.0	321	9	US-10-116-722A-4
14	863.5	36.9	480	9	US-09-526-043-13
15	861.5	36.8	726	9	US-10-072-036-71
16	861	36.8	480	9	US-10-059-585-39
17	861	36.8	480	9	US-09-526-043-14
18	861	36.8	480	10	US-09-771-161A-223
19	861	36.8	480	10	US-09-970-000-4

20	861	36.8	492	9	US-09-955-999-96	Sequence 96, Appl
21	861	36.8	727	9	US-10-072-036-139	Sequence 139, App
22	845	36.1	319	9	US-10-116-722A-8	Sequence 8, Appli
23	843.5	36.0	320	9	US-10-116-722A-5	Sequence 5, Appli
24	842	36.0	319	9	US-10-116-722A-6	Sequence 6, Appli
25	838	35.8	480	10	US-09-205-658-157	Sequence 157, App
26	829.5	35.4	320	9	US-10-116-722A-7	Sequence 7, Appli
27	814	34.8	546	10	US-09-205-658-155	Sequence 155, App
28	801.5	34.3	541	10	US-09-205-658-154	Sequence 154, App
29	791.5	33.8	672	8	US-08-681-219-29	Sequence 29, Appl
30	787	33.6	322	9	US-10-116-722A-2	Sequence 2, Appli
31	784	33.5	637	10	US-09-817-310-2	Sequence 2, Appli
32	780.5	33.4	916	9	US-10-072-036-73	Sequence 73, Appl
33	778.5	33.3	737	10	US-09-771-161A-195	Sequence 4, Appli
34	776	33.2	737	10	US-09-771-161A-195	Sequence 195, App
35	774.5	33.1	587	9	US-10-097-340-256	Sequence 256, App
36	758.5	32.4	584	10	US-09-842-307-2	Sequence 2, Appli
37	746	31.9	483	10	US-09-205-658-156	Sequence 156, App
38	742.5	31.7	740	10	US-09-771-161A-265	Sequence 265, App
39	742.5	31.7	740	10	US-09-771-161A-266	Sequence 266, App
40	742	31.7	311	9	US-10-116-722A-3	Sequence 3, Appli
41	732.5	31.3	824	10	US-09-801-368-312	Sequence 312, App
42	729.5	31.2	375	9	US-10-116-722A-1	Sequence 1, Appli
43	723	30.9	140	10	US-09-925-300-1800	Sequence 1800, Ap
44	714	30.5	584	9	US-10-029-905-10	Sequence 10, Appl
45	713.5	30.5	194	10	US-09-784-249-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-981-353-7
; Sequence 7, Application US/09981353
; Patent No. US0020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 3819039CD1
US-09-981-353-7

Query Match	92.1%	Score	2154;	DB	9;	Length	431;
Best Local Similarity	99.8%	Pred. No.	1.8e-145;				
Matches	406;	Conservative	1;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	39	LAFMKORRMGLNDFIOKIANNYSACKHPEVQSTLKISQPOPELMMANPSPSPSQOIN	98				
Db	25	IAPMKORRMGLNDFIOKIANNYSACKHPEVQSTLKISQPOPELMMANPSPSPSQOIN	84				
QY	99	LGPSSNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEKHIM	158				
Db	85	LGPSSNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEKHIM	144				
QY	159	SERNVLKNNKVPFLVGLHFSPTADKLYFVLDYINGGELFYHLQRCERCFLEPRARYAA	218				
Db	145	SERNVLKNNKVPFLVGLHFSPTADKLYFVLDYINGGELFYHLQRCERCFLEPRARYAA	204				
QY	219	ETASALGYLHSLNIVYRDLKPNILDSQGHIVLTDGFLCKENIEHNSTTSTTCGTPPEYL	278				
Db	205	ETASALGYLHSLNIVYRDLKPNILDSQGHIVLTDGFLCKENIEHNSTTSTTCGTPPEYL	264				

QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPLQLKPNITNSA 338
 DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPLQLKPNITNSA 324
 QY 339 RHLLEGLLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVPNSGPNDLRH 398
 DB 325 RHLLEGLLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVPNSGPNDLRH 384
 QY 399 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 445
 DB 385 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 431

RESULT 2

US-10-000-039-2
 ; Sequence 2, Application US/10000039
 ; Publication No. US20030003559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WALDEGGER, Florian
 ; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY & LARDNER
 ; STREET: 3000 K Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/000.039
 ; FILING DATE: 04-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/031,295
 ; FILING DATE: 26-FEB-1998
 ; APPLICATION NUMBER: DE 197-08-173.8
 ; FILING DATE: 28-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sandercock, Colin G.
 ; REGISTRATION NUMBER: 31,298
 ; REFERENCE/DOCKET NUMBER: 058315/0123
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 672-5300
 ; TELEFAX: (202) 672-5399
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 431 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-000-039-2

Query Match 91.9%; Score 2150; DB 9; Length 431;
 Best Local Similarity 99.5%; Pred. No. 3.4e-145;
 Matches 405; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 39 LAFNKKORMGLNDFIQKIANNYSACKHPEVOSIIKISQPELMNANPSPPPSQOIN 98
 DB 25 IAFNKKORMGLNDFIQKIANNYSACKHPEVOSIIKISQPELMNANPSPPPSQOIN 84
 QY 99 LGPSSNPHAKSPDFHLKLVIGKSGFKVLLARHKAEEVFYAVKVLQKAILKKKEKHIM 158
 DB 85 LCPSSNPHAKSPDFHLKLVIGKSGFKVLLARHKAEEVFYAVKVLQKAILKKKEKHIM 144
 QY 159 SERNVLLKNVGHFPLVGLHFSFQADKLYFVLVDYINGELFYHLQRCFCLEPRARFYAA 218

DB 145 SERNVLLKNVGHFPLVGLHFSFQADKLYFVLVDYINGELFYHLQRCFCLEPRARFYAA 204
 QY 219 ETASALGYLHSLNIVYRDLKPNILNDSQGHIVLTDGGLCKENIEHNSTTSTFCGTPEYL 278
 DB 205 ETASALGYLHSLNIVYRDLKPNILNDSQGHIVLTDGGLCKENIEHNSTTSTFCGTPEYL 264
 QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPLQLKPNITNSA 338
 DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPLQLKPNITNSA 324
 QY 339 RHLLEGLLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVPNSGPNDLRH 398
 DB 325 RHLLEGLLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVPNSGPNDLRH 384
 QY 399 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 445
 DB 385 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 431

RESULT 3

US-09-810-808-5
 ; Sequence 5, Application US/09810808
 ; Patent No. US20020042114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice
 ; Guegler, Karl J.
 ; Hawkins, Phillip R.
 ; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/810,808
 ; FILING DATE: 15-Mar-2001
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/541,228
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0118 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 431 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; IMMEDIATE SOURCE:
 ; LIBRARY: <Unknown>
 ; CLONE: Consensus
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-810-808-5

Query Match 91.7%; Score 2146; DB 10; Length 431;
 Best Local Similarity 99.5%; Pred. No. 6.6e-145;
 Matches 405; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 39 LAFNKKORMGLNDFIQKIANNYSACKHPEVOSIIKISQPELMNANPSPPPSQOIN 98

Db 25 IAFKQRRMGLNDFIOKIANNYSACKHPEVQSILKISQOPELNMNANPPSPPSQOIN 84
 Qy 99 LGPSSNPHAKPSDFHFLKVIKSGSGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 158
 Db 85 LGPSSNPHAKPSDFHFLKVIKSGSGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 144
 Qy 159 SERNVLLKNVKGHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCERCFLEPRARYAA 218
 Db 145 SERNVLLKNVKGHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCERCFLEPRARYAA 204
 Qy 219 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
 Db 205 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
 Qy 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYDNLNKPQLKPNITNSA 338
 Db 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYDNLNKPQLKPNITNSA 324
 Qy 339 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPVNSGPNDLRH 398
 Db 325 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPVNSGPNDLRH 384
 Qy 399 FDEPTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 445
 Db 385 FDEPTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 431

RESULT 4

US-09-810-808-9
 ; Sequence 9, Application US/09810808
 ; Patent No. US20020042114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice
 ; Guegler, Karl J.
 ; Hawkins, Phillip R.
 ; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/810,808
 ; FILING DATE: 15-Mar-2001
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/541,228
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0118 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 430 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 294637
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-810-808-9

Query Match 89.8%; Score 2100.5; DB 10; Length 430;
 Best Local Similarity 97.1%; Pred. No. 1.1e-141;
 Matches 395; Conservative 7; Mismatches 4; Indels 1; Gaps 1;
 Qy 39 LAFMKQRRMGLNDFIOKIANNYSACKHPEVQSILKISQOPELNMNANPPSPPSQOIN 98
 Db 25 IAFKQRRMGLNDFIOKIANNYSACKHPEVQSILKISQOPELNMNANPPSPPSQOIN 84
 Qy 99 LGPSSNPHAKPSDFHFLKVIKSGSGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 158
 Db 85 LGPSSNPHAKPSDFHFLKVIKSGSGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 144
 Qy 159 SERNVLLKNVKGHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCERCFLEPRARYAA 218
 Db 145 SERNVLLKNVKGHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCERCFLEPRARYAA 204
 Qy 219 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
 Db 205 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
 Qy 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYDNLNKPQLKPNITNSA 338
 Db 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYDNLNKPQLKPNITNSA 323
 Qy 339 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPVNSGPNDLRH 398
 Db 324 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPVNSGPNDLRH 383
 Qy 399 FDEPTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 445
 Db 384 FDEPTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 430

RESULT 5

US-09-784-249-2
 ; Sequence 2, Application US/09784249
 ; Patent No. US20010027184A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sanjay Kumar
 ; APPLICANT: Cheng Zou
 ; TITLE OF INVENTION: SERINE/THREONINE PROTEIN KINASE (H-SGK2)
 ; FILE REFERENCE: GH-70124-C1
 ; CURRENT APPLICATION NUMBER: US/09/784,249
 ; CURRENT FILING DATE: 2001-02-15
 ; PRIOR APPLICATION NUMBER: 08/997,212
 ; PRIOR FILING DATE: 1997-12-23
 ; PRIOR APPLICATION NUMBER: 60/051,446
 ; PRIOR FILING DATE: 1997-07-01
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 496
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 ; ORGANISM: HOMO SAPIENS
 ; US-09-784-249-2
 Query Match 63.3%; Score 1481; DB 10; Length 496;
 Best Local Similarity 67.7%; Pred. No. 1.4e-97;
 Matches 281; Conservative 52; Mismatches 68; Indels 14; Gaps 3;
 Qy 41 FMKQRRMGLNDFIOKIANNYSACKHPEVQSILKISQOPELNMNANPPSPPP----- 91
 Db 86 FIKQRRAGLNEFIQNLVRYPELYKHPDVRFLQMDSPKH-----QSDFSEDESSQKLH 141
 Qy 92 SPSQQINLGPSSNPHAKPSDFHFLKVIKSGSGKVLARHKAEEVFYAVKVLQKAILKK 151
 Db 142 STSQINLGPSSNPHAKPSDFHFLKVIKSGSGKVLARHKAEEVFYAVKVLQKIVLNR 201
 Qy 152 KEKHHIMSERNVLLKNVKGHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCERCFLEP 211
 Db 202 KEQHHIMAEARNVLLKNVKGHPFLVGLHYSFQTTEKLYFVLDVFNNGELFFHLQERSFPPEH 261

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QY 212 RARFYAAEIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGGLCKENIEHNSTTSTF 271
Db 262 RARFYAAEIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGGLCKEGIAISDTTTF 321
QY 272 CGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKLQK 331
Db 322 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYNILHKLPSLR 381
QY 332 PNITNSARHLEGLLQKDRKRLGAKDDFMEIKSHVFFSLINWDDLLINKKITPPFPNVS 391
Db 382 PGVSLTAWSIIEELLELDXDRNRLGAKEDFLEIQNHPPFESLWADLVQKKIPPPFPNVA 441
QY 392 GPNDLRFDFEFTPEEPVNSIGKSPDSVLTASVKEAAEAFGLGFSYAPPT-DSFL 445
Db 442 GPDIRNFDFTAFTEETVPYSCVSSDIYNASVLEADDAFVGFYSAPPSEDULF 496

RESULT 6
US-09-971-118-2
; Sequence 2, Application US/09971118
; Patent No. US20020123056A1
; GENERAL INFORMATION:
; APPLICANT: DELANEY, ALLEN
; APPLICANT: YOGANATHAN, THILLAINATHAN
; TITLE OF INVENTION: SGK2 AND ITS USES
; FILE REFERENCE: KINE025CIP
; CURRENT APPLICATION NUMBER: US/09/971.118
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/21479
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/237,419
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-118-2
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Query Match 60.3%; Score 1411; DB 10; Length 367;
Best Local Similarity 71.2%; Pred. No. 9.4e-93;
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;

QY 83 MNANP--SPPPSPSQ---QINLGPSSNPHAKPSDFHLKVIKGSPKVLARHKAEEVF 137
Db 1 MNSSPAGTSPQPSRANGNINLGPANPNAPQTFDFLKVIGKNGYGVLLAKRKSDGAF 60

QY 138 YAVKVLQKATLKKKEKHIMSERNVLLKNVGHFPLVGLHFSFOTADKLYFVLVDYINGGE 197
Db 61 YAVKVLQKSLTKKKEQSHMAEKSVLLKNVRHFPFLVGLRYSFOTPEKLYFVLVDYINGGE 120

QY 198 LFYHLQRCFLPEPRARYAAEIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGFL 257
Db 121 LFYHLQRCFLPEPRARYAAEIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGFL 180

QY 258 CKENIEHNSTSTFCGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTA 317
Db 181 CKGEVEPEDTSTFCGTPEYLAPEVLKPEYDRAVDWCLGAVLYEMLYGLPPFYSQDVS 240

QY 318 EWDYNILNKLPLQKPNITNSARHLEGLLQKDRKRLGAKDDFMEIKSHVFFSLINWDDL 377
Db 241 QMYENILHQPQIPIGGRTVAQKTLQSLHKKQKRLGSKADFLFIKNHVFSPINWDDL 300

QY 378 INKXITPPFPNVSQPNDRHDFEFTPEEPVNSIGKSPDSVLTASVKEAAEAFGLGFSY 437
Db 301 YHKELTPFPNVTGADLKHDFEFTQEAQVSKSIGCTPTDV---ASSSGASSAFLGFSY 357

QY 438 APPTDSFL 445
Db 358 APEDDDIL 365
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RESULT 7
US-09-764-868-669
; Sequence 669, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN ET AL.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 669
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (17)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (181)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (233)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (254)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-669
```

```
Query Match 41.4%; Score 968.5; DB 9; Length 276;
Best Local Similarity 70.9%; Pred. No. 1.9e-61;
Matches 180; Conservative 31; Mismatches 42; Indels 1; Gaps 1;

QY 193 INGGELFYHLQRCFLPEPRARYAAEIASALGYLHSLNIVYRDLPENILDSQGHIVL 252
Db 23 VNGGELFFHLQRCSPFPRARYAAEIASALGYLHSLNIVYRDLPENILDSQGHIVL 82

QY 253 TDFGLCKENIEHNSTSTFCGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFY 312
Db 83 TDFGLCKEGIAISDTTTFCGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFY 142

QY 313 SRNTAEMYNILNKLPLQKPNITNSARHLEGLLQKDRKRLGAKDDFMEIKSHVFFSLI 372
Db 143 CRDVAEMYNILHKLPSLRPGVSLTAWSIIEELLELDXDRNRLGAKEDFLEIQNHPPFESL 202

QY 373 NWDDLINKKITPPFPNVSQPNDRHDFEFTPEEPVNSIGKSPDSVLTASVKEAAEAF 432
Db 203 SWADLVQKKIPPPFPNVSQPNDRHDFEFTPEEPVNSIGKSPDSVLTASVKEAAEAF 262

QY 433 LGFSYAPPT-DSFL 445
Db 263 VGFYSAPPSEDULF 276
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RESULT 8
US-09-771-161A-246
; Sequence 246, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
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QY	79	EPBLMNPSPSPSPQINLG----	PSNPHAK----	PSDHFHLKVIWKGSPQKVLARH	131
DB	113	EEERNMNCSP-----	SQDNTGEEMDASTTHHKKTWNDFDYLKLLGKTGKVLVRE	167	
QY	132	KAEVYFAVQLQKAILKKKEEKHIMSEBNNVLLKNVHPFLVLGLHFSPQTADKLYFVLD		191	
DB	168	KASGKYVAMTLKKEVITAKDEVAHTLTESRY- LKNTRHPPFITSLSKYSPOTKRLCGFVME		226	

; CURRENT APPLICATION NUMBER: US/10/116,722A
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/281,213
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Drosophila sp.
US-10-116-722A-4

Query Match 38.0%; Score 889; DB 9; Length 321;
Best Local Similarity 56.9%; Pred. No. 1e-55;
Matches 170; Conservative 43; Mismatches 84; Indels 2; Gaps 2;

QY 111 DFHFLKVIKSGFGKVLARHKAEEVFYAVKVLQKAILKKKEKHIMSERVLLKNVXH 170
DB 14 NFELKVLGKGTGKVLCKREKATAKAIKILKEVILQKDEVAHTLTESRV-LKSTNH 72

QY 171 PFVLGLHFSQTADKLYFVLVDYINGGELFYHLQRCFCLEPRARFYAAEIASALGYLHSL 230
DB 73 PFLISLKYSPQNDRLCFVMQVYNGGELFWHLHERIFTEDRTRFYGAETISALGYLHSQ 132

QY 231 NIYVRLKPNILLDSQGHIVLTDGFLCKENIEHNSTSTFCGTPPEYLAPEVHLKQPYDR 290
DB 133 GIIYRLKLENLLDKDGHIXITDGLCKEGISDCAATMKTFCGTPPEYLAPEV 192

QY 291 TVDWCLGAVLYEMLYGLPPFYSRNTAEYDNLKPLQKPNITNSARHLLEGLQKOR 350
DB 193 AVDWGTGVVYEMICRGLPFYNRDHDVFLTLVVEVFPKPRNITDAKLLAGLAKOP 252

QY 351 TKRL-GAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPVSGPNDLRFDPFTTEBPV 408
DB 253 KXRLGGKDDVKEIQAHFPFASINWTDVLKIPPPKQVTSDDTDTRYEDKFTGESV 311

RESULT 14
US-09-526-043-13
; Sequence 13, Application US/09526043
; Publication No. US20030100049A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-526-043-13

Query Match 36.9%; Score 863.5; DB 9; Length 480;
Best Local Similarity 42.6%; Pred. No. 1.1e-53;
Matches 182; Conservative 70; Mismatches 138; Indels 37; Gaps 7;

QY 18 RPR-----HKRAEAKRS-----ESFLSGLAFMKORRMGLNDFIOK----- 55
DB 23 RPRYFLKSGSFIGYKERPEADQTLPLPLNFSVAECQLMKTFRPRNFTVIRCLQWTT 82

QY 56 IANNSYACKHPE-----VQSILKISQPEPELMNANSPSPSPSQINLGPSSN 104
DB 83 VIERTHVSPDEREWMRAIQVANSLKORAGPEPMYKCGSPSDSSTTEEMEVAVSK 142

QY 105 PHAK--PSDFHFLKVIKSGFGKVLARHKAEEVFYAVKVLQKAILKKKEKHIMSERN 162
DB 143 ARAKAVTMNDFYLVKLGKGTGKVLVREKATGRYVAMKILRKEVILAKDEVAHTVTESR 202

QY 163 VLLKNVKBPLVGLHFSFOTADKLYFVLVDYINGGELFYHLQRCFCLEPRARFYAAEIAS 222
DB 203 V-LQNRHHPFLTALKYAFQTHDRLCFVMEYANGGELFFHLRSRVFTEERARFYGAETVS 261

QY 223 ALGYLHSLNIYVRLKPNILLDSQGHIVLTDGFLCKENIEHNSTSTFCGTPPEYLAPEV 282
DB 262 ALEYLHSDRVYRDIKLENMLDKDGHIXITDGLCKEGISDCAATMKTFCGTPPEYLAPEV 321

QY 283 LHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLKPLQKPNITNSARHL 342
DB 322 LEDNDYGRAVDWMLGVLVYEMMCGRLPFYQNDHERLFELILMEERFPRTLSPKAKSL 381

QY 343 EGLQLQDRTKRL-GAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPVSGPNDLRFDP 401
DB 382 AGLKKDKPQRLGGGSDAKEVNEHRFFLSINQDVVQKKLLPPFPQVTSDEVDTRYFDD 441

QY 402 ETEEPV 408
DB 442 EFTAQSI 448

RESULT 15
US-10-072-036-71
; Sequence 71, Application US/10072036
; Publication No. US20030082564A1
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP
; APPLICANT: Sara BJORN
; APPLICANT: Soren TULLIN
; APPLICANT: Kasper ALMHOLT
; APPLICANT: Kurt SCUDDER
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0120P
; CURRENT APPLICATION NUMBER: US/10/072,036
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/417,197
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 71
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PKB-EGFP fusion
US-10-072-036-71

Query Match 36.8%; Score 861.5; DB 9; Length 726;
Best Local Similarity 41.9%; Pred. No. 2.4e-53;
Matches 191; Conservative 76; Mismatches 144; Indels 45; Gaps 11;

QY 18 RPRHKKRAEAKRSSEFLSGLAFMKORRMGLNDFIOK-----IANNSYACKHPE---- 67
DB 41 RPQDVQOREAP--LNNFSVAQQLMKTFRPRNFTVIRCLQWTTVIERFHVETPEREE 98

QY 68 ----VQSILKISQPEPELMNANSPSPSPS-----QQINLGPSSNPHAKP-----SDFH 113
DB 99 WTTAIQTADVGLKKQEEEMDFRSGSPSDNSGAEEEMVSL-----AKPKHRTVWNEFE 151

QY 114 FLKVIKSGFGKVLARHKAEEVFYAVKVLQKAILKKKEKHIMSERVLLKNVKBPL 173
DB 152 YLKLKLGKGTGKVLVREKATGRYVAMKILRKEVILAKDEVAHTLTTE-NRVLQNSRHPFL 210

QY 174 VGLHFSFOTADKLYFVLVDYINGGELFYHLQRCFCLEPRARFYAAEIASALGYLHS-LNI 232
DB 211 TALKYSFQTHDRLCFVMEYANGGELFFHLRSRVFSEDRARFYGAETIVSALDYLHSEKNV 270

QY 233 VYRDLKPNILLDSQGHIVLTDGFLCKENIEHNSTSTFCGTPPEYLAPEVHLKQPYDRV 292

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Db      ||||| |::| ||| :||| ||| : | ||||| ||||| | |
271 VYRDLKLENLMLDKDGHKIDFGLCCKEGIKDGATMKTFCGTPYLAPVLEDNDYGRAV 330

Qy      ||||| |::| ||| :||| ||| : | ||||| ||||| | |
293 DMWCLGAVLYEMLYGLPPFYSRNTAEMYNILANKPLQKFNITNSARHLLGLLOKDRYK 352

Db      ||||| |::| ||| :||| ||| : | ||||| ||||| | |
331 DMWGLGVVYEMMCGRLFFYNQDHEKLFELILMEEIRFPRTLGPFAKSLLSGLLKDPKQ 390

Qy      ||||| |::| ||| :||| ||| : | ||||| ||||| | |
353 RL-GAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPNVSGPNDLRHFDPEFTPEPVPNS 411

Db      ||||| |::| ||| :||| ||| : | ||||| ||||| | |
391 RLGGSEDAKEIMQHRFFAGIVQHVYKLSPPFPKQVTSQVTSQVTSQVTSQVTSQVTS 450

Qy      ||||| |::| ||| :||| ||| : | ||||| ||||| | |
412 IGKSPDSVLVTASVKEAAEAPLGFSA-----PP 440

Db      ||||| |::| ||| :||| ||| : | ||||| ||||| | |
451 PPQDDSMCECVD--ERRPHFPQFSYSASSTASDPP 484

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Search completed: June 20, 2003, 19:36:27
Job time : 53 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:23:23 ; Search time 27 Seconds
(without alignments)
484.933 Million cell updates/sec

Title: US-10-067-977-2
Perfect score: 2340
Sequence: 1 MGENQALARLESLLRPR.....KEAAEPLGFSYAPPTDSTFL 445

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2150	91.9	431	4	US-09-031-295-2
2	2146	91.7	431	2	US-08-712-709-5
3	2146	91.7	431	3	US-09-111-444-5
4	2146	91.7	431	4	US-09-541-228-5
5	2100.5	89.8	430	2	US-08-712-709-9
6	2100.5	89.8	430	3	US-09-111-444-9
7	2100.5	89.8	430	4	US-09-541-228-9
8	861	36.8	480	3	US-09-091-058-2
9	810.5	34.6	482	4	US-09-430-564-2
10	810.5	34.6	495	4	US-09-430-564-3
11	807	34.5	525	2	US-08-749-902-7
12	807	34.5	525	2	US-08-749-902-8
13	807	34.5	525	4	US-09-430-564-16
14	775	33.1	671	6	5266464-2
15	774.5	33.1	587	1	US-08-313-274-2
16	696.5	29.8	350	4	US-09-457-040B-37
17	696.5	29.8	351	4	US-09-457-040B-6
18	695	29.7	1151	4	US-09-457-040B-11
19	694.5	29.7	676	4	US-09-313-930-2
20	669.5	28.6	264	2	US-07-857-224B-15
21	666.5	28.5	264	2	US-07-857-224B-10
22	666	28.5	268	4	US-09-430-564-12
23	665.5	28.4	264	2	US-07-857-224B-12
24	661.5	28.3	263	2	US-07-857-224B-13
25	661.5	28.3	264	2	US-07-857-224B-17
26	658	28.1	269	2	US-07-857-224B-14
27	657.5	28.1	264	2	US-07-857-224B-11

28	654	27.9	269	2	US-07-857-224B-16
29	649.5	27.8	258	4	US-09-430-564-6
30	636.5	27.2	260	2	US-07-857-224B-4
31	632.5	27.0	260	2	US-07-857-224B-3
32	624.5	26.7	260	2	US-07-857-224B-2
33	620.5	26.5	260	2	US-07-857-224B-8
34	618.5	26.4	260	2	US-07-857-224B-1
35	612.5	26.2	260	2	US-08-061-636-4
36	612.5	26.2	260	2	US-07-857-224B-6
37	612.5	26.2	260	5	PCT-US94-05268-4
38	610.5	26.1	260	2	US-07-857-224B-7
39	608.5	26.0	272	3	US-08-908-332-8
40	561	24.0	556	2	US-09-016-000-4
41	559	23.9	900	2	US-08-630-822A-62
42	559	23.9	900	2	US-09-005-069-62
43	559	23.9	900	4	US-09-171-156A-21
44	557.5	23.8	258	2	US-07-857-224B-5
45	549	23.5	416	4	US-09-457-040B-10

ALIGNMENTS

RESULT 1
US-09-031-295-2
; Sequence 2, Application US/09031295
; Patent No. 6326181
; GENERAL INFORMATION:
; APPLICANT: LANG, Florian
; APPLICANT: WALDEGGER, Tubingen
; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,295
; FILING DATE: 26-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 197-08-173.8
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercok, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 058315/0123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-031-295-2

Query Match 91.9%; Score 2150; DB 4; Length 431;
Best Local Similarity 99.5%; Pred. No. 1.1e-194;
Matches 405; Conservative 0; Indels 0; Gaps 0;

Qy 39 LAFMKRRMGLNDFIQKIANNYSACKHPEVQSILKISQPELMNANPPSPSQIN 98
Db 25 IAFMKRRMGLNDFIQKIANNYSACKHPEVQSILKISQPELMNANPPSPSQIN 84

QY 99 LGPSSNPHAKPSDFHFLKVIKSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 158
DB 85 LGPSSNPHAKPSDFHFLKVIKSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 144
QY 159 SERNVLLKNVKHPLVLGLHFSFOTADKLYFVLDYINGGELFYHLQRCERCFLEPRARFYAA 218
DB 145 SERNVLLKNVKHPLVLGLHFSFOTADKLYFVLDYINGGELFYHLQRCERCFLEPRARFYAA 204
QY 219 EIASALGYLHSLNIVYRDLKPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVYRDLKPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNIILNKPLQKPNITNSA 338
DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNIILNKPLQKPNITNSA 324
QY 339 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPVNSGPNLDRH 398
DB 325 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPVNSGPNLDRH 384
QY 399 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 445
DB 385 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 431

RESULT 2

US-08-712-709-5
; Sequence 5, Application US/08712709
; Patent No. 5863780
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE: Filed Herewith
; APPLICATION NUMBER: US/08/712,709
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus

US-08-712-709-5

Query Match 91.7%; Score 2146; DB 2; Length 431;
Best Local Similarity 99.5%; Pred. No. 2.6e-194;
Matches 405; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 39 LAFMKORRMGLNDFIOKIANNSSYACKHPEVQSILKISQOEPELMNANSPPPSPSQOIN 98
DB 25 LAFMKORRMGLNDFIOKIANNSSYACKHPEVQSILKISQOEPELMNANSPPPSPSQOIN 84
QY 99 LGPSSNPHAKPSDFHFLKVIKSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 158
DB 85 LGPSSNPHAKPSDFHFLKVIKSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 144
QY 159 SERNVLLKNVKHPLVLGLHFSFOTADKLYFVLDYINGGELFYHLQRCERCFLEPRARFYAA 218
DB 145 SERNVLLKNVKHPLVLGLHFSFOTADKLYFVLDYINGGELFYHLQRCERCFLEPRARFYAA 204
QY 219 EIASALGYLHSLNIVYRDLKPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVYRDLKPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNIILNKPLQKPNITNSA 338
DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNIILNKPLQKPNITNSA 324
QY 339 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPVNSGPNLDRH 398
DB 325 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPVNSGPNLDRH 384
QY 399 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 445
DB 385 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 431

RESULT 3

US-09-111-444-5
; Sequence 5, Application US/09111444
; Patent No. 6045792
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/111,444
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:

LIBRARY: Consensus
US-09-111-444-5

Query Match 91.7%; Score 2146; DB 3; Length 431;
Best Local Similarity 99.5%; Pred. No. 2.6e-194;
Matches 405; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 39 LAFWKQRMGLNDFIQKIANNYSACKHPEVQSILKISQOPEPELMNANPPSPSPSQOIN 98
DB 25 IAFWKQRMGLNDFIQKIANNYSACKHPEVQSILKISQOPEPELMNANPPSPSPSQOIN 84

QY 99 LQSSNPAPKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 158
DB 85 LQSSNPAPKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 144

QY 159 SERNVLLKNVKGHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCERCFLEPRARYAA 218
DB 145 SERNVLLKNVKGHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCERCFLEPRARYAA 204

QY 219 EIASALGYLHSLNIVYRDLKPNILDSQGHIVLTDGCLCKENIEHNSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVYRDLKPNILDSQGHIVLTDGCLCKENIEHNSTTSTFCGTPEYL 264

QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLQKENITNSA 338
DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLQKENITNSA 324

QY 339 RHLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFNPVNSGPNLDRH 398
DB 325 RHLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFNPVNSGPNLDRH 384

QY 399 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEFLGFSYAPPTDSFL 445
DB 385 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEFLGFSYAPPTDSFL 431

RESULT 4

US-09-541-228-5
Sequence 5, Application US/09541228
Patent No. 6232077
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/541.228
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4186
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY:

CLONE: Consensus

US-09-541-228-5

Query Match 91.7%; Score 2146; DB 4; Length 431;
Best Local Similarity 99.5%; Pred. No. 2.6e-194;
Matches 405; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 39 LAFWKQRMGLNDFIQKIANNYSACKHPEVQSILKISQOPEPELMNANPPSPSPSQOIN 98
DB 25 IAFWKQRMGLNDFIQKIANNYSACKHPEVQSILKISQOPEPELMNANPPSPSPSQOIN 84

QY 99 LQSSNPAPKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 158
DB 85 LQSSNPAPKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 144

QY 159 SERNVLLKNVKGHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCERCFLEPRARYAA 218
DB 145 SERNVLLKNVKGHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCERCFLEPRARYAA 204

QY 219 EIASALGYLHSLNIVYRDLKPNILDSQGHIVLTDGCLCKENIEHNSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVYRDLKPNILDSQGHIVLTDGCLCKENIEHNSTTSTFCGTPEYL 264

QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLQKENITNSA 338
DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLQKENITNSA 324

QY 339 RHLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFNPVNSGPNLDRH 398
DB 325 RHLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFNPVNSGPNLDRH 384

QY 399 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEFLGFSYAPPTDSFL 445
DB 385 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEFLGFSYAPPTDSFL 431

RESULT 5

US-08-712-709-9
Sequence 9, Application US/08712709
Patent No. 5863780
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 294637
US-08-712-709-9

Query Match 89.8%; Score 2100.5; DB 2; Length 430;
Best Local Similarity 97.1%; Pred. No. 5.1e-190;
Matches 395; Conservative 7; Mismatches 4; Indels 1; Gaps 1;
QY 39 LAFMKORRMGLNDFIOKIANNYSACKHPEVOSILKISQPOPELNMNANSPSPSOQIN 98
DB 25 IAFMKORRMGLNDFIOKLANNYSACKHPEVOSYLYKISQPOPELNMNANSPSPSOQIN 84
QY 99 LQSSNPHAKPSDFHFLKVIKSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 158
DB 85 LQSSNPHAKPSDFHFLKVIKSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 144
QY 159 SERNVLLKNVHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCFCLEPRARFYAA 218
DB 145 SERNVLLKNVHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCFCLEPRARFYAA 204
QY 219 EIASALGYLHSLNIVRDLPENILDSQGHVLTDFGLCKENIEHNSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVRDLPENILDSQGHVLTDFGLCKENIEHNSTTSTFCGTPEYL 264
QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLK-NITNSA 338
DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLK-NITNSA 323
QY 339 RHLLEGLLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFPNPNVSGPDLRH 398
DB 324 RHLLEGLLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFPNPNVSGPDLRH 383
QY 399 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLGSYAPPTDSFL 445
DB 384 FDPEFTEEPVSSIGRSPDSILVTASVKEAAEAFGLGSYAPPTDSFL 430

RESULT 6

US-09-111-444-9
Sequence 9, Application US/09111444
Patent No. 6045792
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111.444
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 294637
US-09-111-444-9
Query Match 89.8%; Score 2100.5; DB 3; Length 430;
Best Local Similarity 97.1%; Pred. No. 5.1e-190;
Matches 395; Conservative 7; Mismatches 4; Indels 1; Gaps 1;
QY 39 LAFMKORRMGLNDFIOKIANNYSACKHPEVOSILKISQPOPELNMNANSPSPSOQIN 98
DB 25 IAFMKORRMGLNDFIOKLANNYSACKHPEVOSYLYKISQPOPELNMNANSPSPSOQIN 84
QY 99 LQSSNPHAKPSDFHFLKVIKSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 158
DB 85 LQSSNPHAKPSDFHFLKVIKSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 144
QY 159 SERNVLLKNVHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCFCLEPRARFYAA 218
DB 145 SERNVLLKNVHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCFCLEPRARFYAA 204
QY 219 EIASALGYLHSLNIVRDLPENILDSQGHVLTDFGLCKENIEHNSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVRDLPENILDSQGHVLTDFGLCKENIEHNSTTSTFCGTPEYL 264
QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLK-NITNSA 338
DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLK-NITNSA 323
QY 339 RHLLEGLLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFPNPNVSGPDLRH 398
DB 324 RHLLEGLLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFPNPNVSGPDLRH 383
QY 399 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLGSYAPPTDSFL 445
DB 384 FDPEFTEEPVSSIGRSPDSILVTASVKEAAEAFGLGSYAPPTDSFL 430

RESULT 7

US-09-541-228-9
Sequence 9, Application US/09541228
Patent No. 6232077
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA: US/09/541,228
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 294637
US-09-541-228-9

Query Match 89.8%; Score 2100.5; DB 4; Length 430;
Best Local Similarity 97.1%; Pred. No. 5.1e-190;
Matches 395; Conservative 7; Mismatches 4; Indels 1; Gaps 1;

QY 39 LAPKQRMGLNDFIQIANNVACKHPEVOSILKISQOPEPELMNANPSPSPSQOIN 98
DB 25 IAFMKQRMGLNDFIQIANNVACKHPEVOSYLYKISQOPEPELMNANPSPSPSQOIN 84
QY 99 LQSSNPAPKSPDFHFLVKVIGKSGFVKVLLARHKAEEVFYAVKVLQKAILKKKEEKHIM 158
DB 85 LQSSNPAPKSPDFHFLVKVIGKSGFVKVLLARHKAEEVFYAVKVLQKAILKKKEEKHIM 144
QY 159 SERNVLKNVKKPFLVGLHFSFOTADKLYFVLDYINGGELFYHLQRCFCLEPRARYAA 218
DB 145 SERNVLKNVKKPFLVGLHFSFOTADKLYFVLDYINGGELFYHLQRCFCLEPRARYAA 204
QY 219 EIASALGYLHSLNIVYRDLKAPENILDSQGHIVLTDGLCKENIEHNSTTTCGTPPEYL 278
DB 205 EIASALGYLHSLNIVYRDLKAPENILDSQGHIVLTDGLCKENIEHNSTTTCGTPPEYL 264
QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 338
DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLK-NITNSA 323
QY 339 RHLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFPNPNVSGPNDLRH 398
DB 324 RHLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFPNPNVSGPNDLRH 383
QY 399 FDEPTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 445
DB 384 FDEPTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 430

RESULT 8

US-09-091-058-2
; Sequence 2, Application US/09091058
; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A.
; APPLICANT: Frech, Matthias
; TITLE OF INVENTION: Screening Method
; FILE REFERENCE: 4-20683/A/20684/PT
; CURRENT APPLICATION NUMBER: US/09/091.058
; CURRENT FILING DATE: 1998-06-10

; EARLIER APPLICATION NUMBER: PCT/EP96/04814
; EARLIER FILING DATE: 1996-11-05
; EARLIER APPLICATION NUMBER: 9525703.6
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-091-058-2

Query Match 36.8%; Score 861; DB 3; Length 480;
Best Local Similarity 42.3%; Pred. No. 5.8e-73;
Matches 189; Conservative 76; Mismatches 144; Indels 38; Gaps 10;

QY 18 RPHKKRAEAOXRSSEFLSLGLAFMKQRRMGLNDFIQK-----IANNVACKHPE----- 67
DB 41 RPQDVQREAP--LNNFSAQCQLMKTERPRNTFIIRCLQWTVTIERTFHVTPEERE 98
QY 68 ---VOSILKISQOPEPELMNANPSPSPSPS---OOINLGPSSNPAPK-----SDFH 113
DB 99 WTTAQTVDGLKKQEEEMDFRSGSPSDNSGAEEVSL-----AKPKHRTVWNEFE 151
QY 114 FLKVGKSGFVKVLLARHKAEEVFYAVKVLQKAILKKKEEKHIMERNVLLKNVKKHPL 173
DB 152 YLKLKLGKGTGKIVLVKATGRYYAMKILKKEVIVAKDEVAHTLTE-NRVLQNSRHPFL 210
QY 174 VGLHFSFOTADKLYFVLDYINGGELFYHLQRCFCLEPRARYAAIASALGYLHSLN 232
DB 211 TALKYSFQTHDRLCFVMEYANGGELFHLRSRVSFSEDRARFYGAIVSALDYLHSEKNV 270
QY 233 VYRDLKAPENILDSQGHIVLTDGLCKENIEHNSTTTCGTPPEYLAPVHLHKQPYDRTV 292
DB 271 VYRDLKAPENILDSQGHIVLTDGLCKENIEHNSTTTCGTPPEYLAPVHLHKQPYDRTV 330
QY 293 DMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSARHLEGLLQKDRTK 352
DB 331 DMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSARHLEGLLQKDRTK 390
QY 353 RL-GAKDDFMEIKSHVFFSLINWDDLKINKITPPFPNPNVSGPNDLRHFDDEPTEEPVNS 411
DB 391 RLGGSGSEDAKEINQHRFFAGIVQHVYKLSPPFKPQVTSFDTTRYFDEEFTAQMITIT 450
QY 412 IGKSPDSVLVTASVKEAAEAFLGFSYA 438
DB 451 PPQDDSMCEVD--ERRPHFPQFSYS 475

RESULT 9

US-09-430-564-2
; Sequence 2, Application US/09430564
; Patent No. 6372467
; GENERAL INFORMATION:
; APPLICANT: John Blenis
; APPLICANT: Kay K. Lee-Fruman
; APPLICANT: Calvin J. Kuo
; TITLE OF INVENTION: P54S6K AND P85S6K GENES, PROTEINS,
; FILE REFERENCE: 00246/506002
; CURRENT APPLICATION NUMBER: US/09/430,564
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/106,141
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-564-2

Query Match 34.6%; Score 810.5; DB 4; Length 482;

Best Local Similarity 44.6%; Pred. No. 3.4e-68;
Matches 173; Conservative 65; Mismatches 111; Indels 39; Gaps 12;

Qy 79 EPELMANPSP-----PPSPSQ-----INLGPSS-NPHAKPSDFHFLKVIGK 120
Db 20 EPELSPADACPLAELRAAGLEPVGHYBEVELTETSVNNGPERICPHC-----FELLRLVIGK 75

Qy 121 GSGFKVLLARHKAEEV---FYAVKVLQKAILKK-KEEKHIMSERVLLKNVKKHPLVG 175
Db 76 GGVKVFQVR-KVQGTNLGKIYAMKVLKAKI VRNAKDTAHTRAERNI-LESVKHGPIVE 133

Qy 176 LHFSFOTADKLYFVLDYINGELFVHLQRECFLEPRARFYAAEIASALGYLHSLNIVYR 235
Db 134 LAYAFQGGKLYLLECLSGGELFHLEREGIFLEDACFYLAETILALGHLHSQGIYR 193

Qy 236 DLKPENILLOSQHIVLTDGLCKENIEHNSSTSTFCGTPEYLAPEVLHQPVDRTVDWW 295
Db 194 DLKPENILLOSQHIVLTDGLCKESIHGAVTHFCGTIEYMAPEILVRSGHNRADWW 253

Qy 296 CLGAVLYEMLYGLPPFYSRNTAEYDNLNKPLOLKNITNSARHLLLEGLOKDRTKRL- 354
Db 254 SLGALMYDMLTGSPPFTAEARRKTKMDKIIRGKLALPYLTPDARDLVKKFLKRNPSORIG 313

Qy 355 GAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNPNVSGPNDLRHFDPEFTEE-PVPNSIG 413
Db 314 GPGDAADVQRHPFFRHHWDDLLAWRDPFPPCLQSEEDVSQFDRFTRQTPV----- 368

Qy 414 KSPDSVLVTASVKEAAEAFGLFSYAPPT 441
Db 369 DSPDD---TALSANQAFLGFTYVAPS 393

RESULT 10
US-09-430-564-3
; Sequence 3, Application US/09430564
; Patent No. 6372467
; GENERAL INFORMATION:
; APPLICANT: John Blenis
; APPLICANT: Kay K. Lee-Fruman
; APPLICANT: Calvin J. Kuo
; TITLE OF INVENTION: P54S6K AND P85S6K GENES, PROTEINS,
; TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
; FILE REFERENCE: 00246/506002
; CURRENT APPLICATION NUMBER: US/09/430,564
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/106,141
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-564-3

Query Match 34.6%; Score 810.5; DB 4; Length 495;
Best Local Similarity 44.6%; Pred. No. 3.6e-68;
Matches 173; Conservative 65; Mismatches 111; Indels 39; Gaps 12;

Qy 79 EPELMANPSP-----PPSPSQ-----INLGPSS-NPHAKPSDFHFLKVIGK 120
Db 33 EPELSPADACPLAELRAAGLEPVGHYBEVELTETSVNNGPERICPHC-----FELLRLVIGK 88

Qy 121 GSGFKVLLARHKAEEV---FYAVKVLQKAILKK-KEEKHIMSERVLLKNVKKHPLVG 175
Db 89 GGVKVFQVR-KVQGTNLGKIYAMKVLKAKI VRNAKDTAHTRAERNI-LESVKHGPIVE 146

Qy 176 LHFSFOTADKLYFVLDYINGELFVHLQRECFLEPRARFYAAEIASALGYLHSLNIVYR 235
Db 147 LAYAFQGGKLYLLECLSGGELFHLEREGIFLEDACFYLAETILALGHLHSQGIYR 206

Qy 236 DLKPENILLOSQHIVLTDGLCKENIEHNSSTSTFCGTPEYLAPEVLHQPVDRTVDWW 295
Db 236 DLKPENILLOSQHIVLTDGLCKENIEHNSSTSTFCGTPEYLAPEVLHQPVDRTVDWW 295

Db 207 DLKPENILLOSQHIVLTDGLCKESIHGAVTHFCGTIEYMAPEILVRSGHNRADWW 266
Qy 296 CLGAVLYEMLYGLPPFYSRNTAEYDNLNKPLOLKNITNSARHLLLEGLOKDRTKRL- 354
Db 267 SLGALMYDMLTGSPPFTAEARRKTKMDKIIRGKLALPYLTPDARDLVKKFLKRNPSORIG 326

Qy 355 GAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNPNVSGPNDLRHFDPEFTEE-PVPNSIG 413
Db 327 GPGDAADVQRHPFFRHHWDDLLAWRDPFPPCLQSEEDVSQFDRFTRQTPV----- 381

Qy 414 KSPDSVLVTASVKEAAEAFGLFSYAPPT 441
Db 382 DSPDD---TALSANQAFLGFTYVAPS 406

RESULT 11
US-08-749-902-7
; Sequence 7, Application US/08749902
; Patent No. 5985635
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
; TITLE OF INVENTION: PROTEIN KINASES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA: US/08/749,902
; APPLICATION NUMBER: US/08/749,902
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0150 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 525 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 189508
US-08-749-902-7

Query Match 34.5%; Score 807; DB 2; Length 525;
Best Local Similarity 46.8%; Pred. No. 8.3e-68;
Matches 164; Conservative 63; Mismatches 105; Indels 20; Gaps 9;

Qy 97 INLGPSSNPHAKPSDFHFLKVIGKSGFGKVLARH-----KAEVVFVAVKVLQKAILKK- 151
Db 79 VNGEPEK---IRPECELELVLGKGGYGVKVFQVKVTGANTGKIP-AMKVLKAMIVRNA 134

Qy 152 KEEKHIMSERVLLKNVKKHPLVGLHFSFOTADKLYFVLDYINGELFVHLQRECFLEP 211
Db 135 KDTAHTKAERNI-LEEVKHPFIVDLIYAFQGGKLYLLEVLGGLFMQLREGIFMED 193

QY 212 RARFYAAEIASALGYLHSLNIVYRDLPENILLDSQGHIVLTFGLCKENIEHNSTSTF 271
 DB 194 TACFYLAELSMALGHLHKGIIYRDLPENIMLNHQHVKLTDFGLCKESIHGTVTHTF 253
 QY 272 CGTPEYLAPVLHQPDRYTDVWCLGAVLYEMLYGLPPFYSRNTAEYDNIILNKPLQLK 331
 DB 254 CGTIEYMAPEILMRSGHNRAVDWWSLGMALMYDMLTGAPPTGENRKKTIIDKILCKLNLP 313
 QY 332 PNITNSARHLLEGLOKDRTRKLG-A-KDDFMEIKSHVFFSLINWDDLINKKITPPFPNPV 390
 DB 314 PYLTQEARDLKLLKRNAAASRLGAGPGDAGEVQAHPFFRHHINWEEELLARKVBPFPKPL 373
 QY 391 SGNDLRHFDPEFTEE-PVPNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPT 441
 DB 374 QSEEDVSQFDSKFTROTTPV-----DSPDDSTLSES---ANQVFLGFTYVAPS 417

RESULT 12

US-08-749-902-8
 ; Sequence 8, Application US/08749902
 ; Patent No. 5985635
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Hillman, Jennifer L.
 ; TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
 ; TITLE OF INVENTION: PROTEIN KINASES
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 2.0
 ; CURRENT APPLICATION DATA: US/08749,902
 ; APPLICATION NUMBER: US/08749,902
 ; FILING DATE: Filed Herewith
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0150 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 525 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 1562
 ; US-08-749-902-8

Query Match 34.5%; Score 807; DB 2; Length 525;
 Best Local Similarity 46.6%; Pred. No. 8.3e-68;
 Matches 164; Conservative 63; Mismatches 105; Indels 20; Gaps 9;
 QY 97 INLGPSNPHAKPSDFHFLKVGKSGFKVLLARH----KAEVYFAVKYLQKAILKK- 151
 DB 79 VNRGPEK---IRPECFELLRLVGLGGYGVQVRKVTGANTGKIF-AMKVLKKAMIVRNA 134

QY 152 KEEKHIMSERNVLLKNVKKHPFLVGLHPSFQTADKLYFVLVDYINGGELFYHLQERCEPLEP 211
 DB 135 KDTAHTKAERNI-LEEVKHPFIVDLIYAFQTQGLKYLILEYLSGGELFMQLEREGIFMED 193
 QY 212 RARFYAAEIASALGYLHSLNIVYRDLPENILLDSQGHIVLTFGLCKENIEHNSTSTF 271
 DB 194 TACFYLAELSMALGHLHKGIIYRDLPENIMLNHQHVKLTDFGLCKESIHGTVTHTF 253
 QY 272 CGTPEYLAPVLHQPDRYTDVWCLGAVLYEMLYGLPPFYSRNTAEYDNIILNKPLQLK 331
 DB 254 CGTIEYMAPEILMRSGHNRAVDWWSLGMALMYDMLTGAPPTGENRKKTIIDKILCKLNLP 313
 QY 332 PNITNSARHLLEGLOKDRTRKLG-A-KDDFMEIKSHVFFSLINWDDLINKKITPPFPNPV 390
 DB 314 PYLTQEARDLKLLKRNAAASRLGAGPGDAGEVQAHPFFRHHINWEEELLARKVBPFPKPL 373
 QY 391 SGNDLRHFDPEFTEE-PVPNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPT 441
 DB 374 QSEEDVSQFDSKFTROTTPV-----DSPDDSTLSES---ANQVFLGFTYVAPS 417

RESULT 13

US-09-430-564-16
 ; Sequence 16, Application US/09430564
 ; Patent No. 6372467
 ; GENERAL INFORMATION:
 ; APPLICANT: John Blenis
 ; APPLICANT: Kay K. Lee-Fruman
 ; APPLICANT: Calvin J. Kuo
 ; TITLE OF INVENTION: P54S6K AND P85S6K GENES, PROTEINS,
 ; FILE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
 ; FILE REFERENCE: 002467/506002
 ; CURRENT APPLICATION NUMBER: US/09/430,564
 ; CURRENT FILING DATE: 1999-10-29
 ; PRIOR APPLICATION NUMBER: 60/106,141
 ; PRIOR FILING DATE: 1998-10-29
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16
 ; LENGTH: 525
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-430-564-16

Query Match 34.5%; Score 807; DB 4; Length 525;
 Best Local Similarity 46.6%; Pred. No. 8.3e-68;
 Matches 164; Conservative 63; Mismatches 105; Indels 20; Gaps 9;

QY 97 INLGPSNPHAKPSDFHFLKVGKSGFKVLLARH----KAEVYFAVKYLQKAILKK- 151
 DB 79 VNRGPEK---IRPECFELLRLVGLGGYGVQVRKVTGANTGKIF-AMKVLKKAMIVRNA 134
 QY 152 KEEKHIMSERNVLLKNVKKHPFLVGLHPSFQTADKLYFVLVDYINGGELFYHLQERCEPLEP 211
 DB 135 KDTAHTKAERNI-LEEVKHPFIVDLIYAFQTQGLKYLILEYLSGGELFMQLEREGIFMED 193
 QY 212 RARFYAAEIASALGYLHSLNIVYRDLPENILLDSQGHIVLTFGLCKENIEHNSTSTF 271
 DB 194 TACFYLAELSMALGHLHKGIIYRDLPENIMLNHQHVKLTDFGLCKESIHGTVTHTF 253
 QY 272 CGTPEYLAPVLHQPDRYTDVWCLGAVLYEMLYGLPPFYSRNTAEYDNIILNKPLQLK 331
 DB 254 CGTIEYMAPEILMRSGHNRAVDWWSLGMALMYDMLTGAPPTGENRKKTIIDKILCKLNLP 313
 QY 332 PNITNSARHLLEGLOKDRTRKLG-A-KDDFMEIKSHVFFSLINWDDLINKKITPPFPNPV 390
 DB 314 PYLTQEARDLKLLKRNAAASRLGAGPGDAGEVQAHPFFRHHINWEEELLARKVBPFPKPL 373
 QY 391 SGNDLRHFDPEFTEE-PVPNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPT 441
 DB 374 QSEEDVSQFDSKFTROTTPV-----DSPDDSTLSES---ANQVFLGFTYVAPS 417

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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:14:32 ; Search time 73 Seconds
(without alignments)
812.281 Million cell updates/sec

Title: US-10-067-977-2

Perfect score: 2340

Sequence: 1 MGEQALARLESLLRPR.....KEAAEAFLGFSYAPPTDSFL 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_101002.*
- 1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
 - 2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
 - 3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
 - 4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
 - 5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
 - 6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
 - 7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
 - 8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
 - 9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
 - 10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
 - 11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
 - 12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
 - 13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
 - 14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
 - 15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
 - 16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
 - 17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
 - 18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
 - 19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
 - 20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
 - 21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
 - 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
 - 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2154	92.1	431	20	AAW90139
2	2150	91.9	431	19	AAW77217
3	2150	91.9	431	21	AAW24115
4	2150	91.9	431	22	AAW65613
5	2146	91.7	431	19	AAW54025
6	2141	91.5	431	21	AAV95279
7	2118	90.5	431	21	AAW24116
8	2118	90.5	431	21	AAV93530
9	2052.5	87.7	430	22	AAW65614
10	1992	85.1	388	20	AAV48573

11	1976	84.4	373	22	AAW99815	AGC protein kinase
12	1699	72.6	321	22	AAW99836	AGC protein kinase
13	1481	63.3	496	20	AAW87772	Human serum glucoc
14	1476	63.1	429	21	AAW95378	Human serum and gl
15	1476	63.1	496	22	AAU87228	Novel central nerv
16	1476	63.1	496	22	AAU87382	Novel central nerv
17	1476	63.1	496	22	AAW40820	Human polypeptide
18	1463	62.5	429	21	AAW24114	Human serine threo
19	1461	62.4	496	22	AAW38834	Human polypeptide
20	1419	60.6	427	21	AAW95376	Human serum and gl
21	1413.5	60.4	382	22	AAW25594	Human protein sequ
22	1411	60.3	367	21	AAW95375	Human serum and gl
23	1411	60.3	367	22	AAU28087	Novel human secret
24	1411	60.3	367	23	AAW22765	Human serum and gl
25	1409	60.2	367	22	AAW65708	Novel protein kina
26	1387	59.3	367	21	AAW95377	Mouse serum and gl
27	1281	54.7	464	22	AAW93732	Human polypeptide
28	1267.5	54.2	319	22	AAW99838	AGC protein kinase
29	1254.5	53.6	322	22	AAW99837	AGC protein kinase
30	1227	52.4	446	22	AAW65616	Novel protein kina
31	968.5	41.4	276	22	AAU87658	Novel central nerv
32	968.5	41.4	276	22	AAU17104	Novel signal trans
33	955.5	40.8	244	22	AAW65615	Novel protein kina
34	916	39.1	479	21	AAW19284	Amino acid sequenc
35	916	39.1	479	21	AAW13393	Human Akt-3. Homo
36	916	39.1	479	23	AAU79420	Human protein kina
37	916	39.1	479	23	ABW06998	Human Akt3 protein
38	912	39.0	465	21	AAW19011	Amino acid sequenc
39	912	39.0	465	22	AAW78018	Human Akt3. Homo
40	912	39.0	465	22	AAW19996	Human serine/threo
41	912	39.0	465	22	AAW19998	Human serine/threo
42	910	38.9	454	22	AAW78021	Akt3 related polyp
43	908	38.8	479	21	AAW43132	Human ORFX ORF2896
44	894	38.2	530	22	AAW66370	Drosophila melanog
45	894	38.2	530	22	ABW71272	Drosophila melanog

ALIGNMENTS

RESULT 1

AAW90139
ID AAW90139 standard; Protein; 431 AA.

XX AC AAW90139;

XX DT 15-MAR-1999 (first entry)

XX DE Human sgk protein.

XX KW Serum glucocorticoid regulated kinase; sgk; human; treatment; inhibitor;

XX KW serine/threonine protein kinase family; antagonist; diabetic nephropathy;

XX KW chronic renal failure; inflammation; Alzheimers disease; wound.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 381 /note= "encoded by GAG"

XX PN EP887081-A2.

XX PD 30-DEC-1998.

XX PF 27-MAY-1998; 98EP-0304189.

XX PR 27-JUN-1997; 97US-0051124.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Kumar JM;

XX DR WPI; 1999-047627/05.

DR N-PSDB; AAV74190.
XX
XX Treating chronic renal failure, diabetic nephropathy and Alzheimer's
PT disease - by administration of nucleic acids and antagonists which
PT inhibit activity or expression of human serum glucocorticoid
PT regulated kinase (sgk), a serine/threonine protein kinase
XX
XX
PS Disclosure; Page 16-17; 17pp; English.
XX
XX This sequence represents a novel human serum glucocorticoid regulated
CC kinase (sgk) protein which is a member of the serine/threonine protein
CC kinase family. This protein is used for the treatment of a subject having
CC need to inhibit/antagonise activity or expression of human sgk
CC polypeptide e.g. for the treatment of chronic renal failure, diabetic
CC nephropathy, inflammation, Alzheimers disease and wounds.
XX
SQ Sequence 431 AA;
Query Match 92.1%; Score 2154; DB 20; Length 431;
Best Local Similarity 99.8%; Pred. No. 2.9e-192;
Matches 406; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 39 LAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQOPELMNANPPSPSQOIN 98
DB 25 IAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQOPELMNANPPSPSQOIN 84
QY 99 LGSNNPHAKPSDFHFLKVGSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 158
DB 85 LGSNNPHAKPSDFHFLKVGSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 144
QY 159 SERVLKQVDPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 218
DB 145 SERVLKQVDPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 204
QY 219 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 338
DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 324
QY 339 RHLLEGLQKQDRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFNPVNSGPNDRH 398
DB 325 RHLLEGLQKQDRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFNPVNSGPNDRH 384
QY 399 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
DB 385 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431
RESULT 2
AAW77217
ID AAW77217 standard; Protein; 431 AA.
XX
XX AAW77217;
XX
DT 16-NOV-1998 (first entry)
XX
DE Human cell-volume regulating kinase h-sgk.
XX
KW Human; cell-volume; kinase; h-sgk; diabetes mellitus;
KW renal insufficiency; inflammation; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN EP861896-A2.
XX
XX
PD 02-SEP-1998.
XX
XX 27-JAN-1998; 98EP-0101338.
XX
XX 28-FEB-1997; 97DE-1008173.
XX

XX
PA (DADE-) DADE BEHRING MARBURG GMBH.
XX
XX Lang F, Waldegger S;
XX
XX WPI; 1998-449109/39.
DR N-PSDB; AAV48311.
XX
XX New nucleic acid encoding cell-volume regulating kinase h-sgk and
PT related proteins - used for diagnosis and treatment of diseases
PT involving changes in cell volume, e.g. renal insufficiency,
PT inflammation, infections etc.
XX
XX Disclosure; Fig 1; 15pp; German.
PS
XX The human cell-volume regulating kinase h-sgk is inhibited by the
CC swelling of cells (or presence of urea), whereas cell shrinkage
CC stimulates its expression. The nucleic acid h-sgk, and fragments, are
CC particularly used to detect changes in cell volume, specifically for
CC diagnosis of conditions that involve such changes, e.g. hyper- and hypo-
CC natriemia, diabetes mellitus, renal insufficiency, hypercatabolism,
CC hepatic encephalopathy, inflammation, microbial/viral infection, fructose
CC intolerance, hyper- and hypo-glycaemia and Alzheimer's disease.
CC The nucleic acid, protein and products including receptors that bind
CC h-sgk, can be used to treat these disorders.
XX
SQ Sequence 431 AA;
Query Match 91.9%; Score 2150; DB 19; Length 431;
Best Local Similarity 99.5%; Pred. No. 6.8e-192;
Matches 405; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 39 LAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQOPELMNANPPSPSQOIN 98
DB 25 IAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQOPELMNANPPSPSQOIN 84
QY 99 LGSNNPHAKPSDFHFLKVGSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 158
DB 85 LGSNNPHAKPSDFHFLKVGSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 144
QY 159 SERVLKQVDPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 218
DB 145 SERVLKQVDPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 204
QY 219 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 338
DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 324
QY 339 RHLLEGLQKQDRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFNPVNSGPNDRH 398
DB 325 RHLLEGLQKQDRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFNPVNSGPNDRH 384
QY 399 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
DB 385 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431
RESULT 3
AAW74115
ID AAW74115 standard; Protein; 431 AA.
XX
XX AAW74115;
XX
XX 29-JAN-2001 (first entry)
DT
XX Human serum and glucocorticoid regulated kinase protein (HSGK).
DE
XX Human; STK3; serine threonine kinase; HSGK; RSGK;
KW serum and glucocorticoid regulated kinase.
KW

XX OS Homo sapiens.
 XX CN1259573-A.
 XX 12-JUL-2000.
 XX 29-OCT-1998; 98CN-0123822.
 XX 29-OCT-1998; 98CN-0123822.
 XX (UYFU-) UNIV FUDAN.
 XX Yu L, Fu Q, Zhao Y;
 XX WPI; 2000-587991/56.
 XX New human serine threonine protein kinase, its code sequence,
 XX preparation, and use -
 XX Example 3; Fig 3; 29pp; Chinese.
 XX The present invention describes human serine threonine kinase STK3,
 XX which is a new member of the serine/threonine protein kinase family.
 XX Human STK3 shares homology with human serum and glucocorticoid
 XX regulated kinase (HSBK) and rat SGK (RSGK). The present sequence
 XX represents the human HSGK protein sequence from the present invention.
 XX SQ Sequence 431 AA;

Query Match 91.9%; Score 2150; DB 21; Length 431;
 Best Local Similarity 99.5%; Pred. No. 6.8e-192;
 Matches 405; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 39 LAFMKQRRMGNDFIQKIANNYSACKHPEVQSILKISQPEPELMNANPPSPSQIN 98
 DB 25 IAFMKQRRMGNDFIQKIANNYSACKHPEVQSILKISQPEPELMNANPPSPSQIN 84
 QY 99 LGPSSNPHAKPSDFHFLKVGSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 158
 DB 85 LGPSSNPHAKPSDFHFLKVGSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 144
 QY 159 SERVLKKNVGHPLFVGLHFSFQTADKLYFVLVDYINGGELFYHLQERCFLEPRARYAA 218
 DB 145 SERVLKKNVGHPLFVGLHFSFQTADKLYFVLVDYINGGELFYHLQERCFLEPRARYAA 204
 QY 219 EIASALGYLHSLNIVYRDLKPNILLDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPPEYL 278
 DB 205 EIASALGYLHSLNIVYRDLKPNILLDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPPEYL 264
 QY 279 APEVLHKQPYDRTVDWVWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLKPNITNSA 338
 DB 265 APEVLHKQPYDRTVDWVWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLKPNITNSA 324
 QY 339 RHLLEGLLQDKRTKRLGAKDPMFEEKSHVFFSLINWDDLKIKITPPFNPNVSGPNDLRH 398
 DB 325 RHLLEGLLQDKRTKRLGAKDPMFEEKSHVFFSLINWDDLKIKITPPFNPNVSGPNELRH 384
 QY 399 FDFEFTPEPNSIGKSPDSVLVTASVKEAAEAPLGFSYAPPTDSFL 445
 DB 385 FDFEFTPEPNSIGKSPDSVLVTASVKEAAEAPLGFSYAPPTDSFL 431

RESULT 4
 AAB65613
 ID AAB65613 standard; Protein; 431 AA.
 XX AAB65613;
 XX 27-MAR-2001 (first entry)
 XX Novel protein kinase, SEQ ID NO: 139.
 XX

KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
 KW dermatological; antidiabetic; antiinfectility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
 XX Homo sapiens.
 XX WO200073469-A2.
 XX 07-DEC-2000.
 XX 26-MAY-2000; 2000WO-US14842.
 XX 28-MAY-1999; 99US-0136503.
 XX (SUGB-) SUGEN INC.
 XX PLOWMAN GD, Martinez R, Whyte D, Sudersanam S;
 XX WPI; 2001-032161/04.
 XX N-PSDB; AAF44639.
 XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 XX treating immune-related diseases and disorders, cardiovascular disease,
 XX neurodegenerative diseases and/or cancers -
 XX Claim 10; Fig 1; 310pp; English.
 XX The present sequence is a novel protein kinase. The novel protein kinases
 XX and the nucleic acids that encode them may be used in the treatment and
 XX diagnosis of diseases associated with inappropriate kinase expression
 XX such as immune-related diseases and disorders, cardiovascular disease,
 XX neurodegenerative diseases and/or cancers. The nucleic acids and
 XX complementary sequences may also be used as DNA probes in diagnostic
 XX assays. The kinase polypeptides may be used as antigens in the production
 XX of antibodies of kinase expression and activity. Anti-kinase antibodies
 XX and kinase antagonists may also be used to down regulate kinase
 XX expression and activity. Diseases related to kinase expression and
 XX activity include rheumatoid arthritis, atherosclerosis, autoimmune
 XX disorders, complications of organ transplantation, myocardial infarction,
 XX immune disorders, cardiomyopathies, strokes, renal failure,
 XX oxidative-stress related disorders, chronic inflammatory bowel disease,
 XX chronic inflammatory pelvic disease, multiple sclerosis, asthma,
 XX osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
 XX reproductive disorders.
 XX SQ Sequence 431 AA;

Query Match 91.9%; Score 2150; DB 22; Length 431;
 Best Local Similarity 99.5%; Pred. No. 6.8e-192;
 Matches 405; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 39 LAFMKQRRMGNDFIQKIANNYSACKHPEVQSILKISQPEPELMNANPPSPSQIN 98
 DB 25 IAFMKQRRMGNDFIQKIANNYSACKHPEVQSILKISQPEPELMNANPPSPSQIN 84
 QY 99 LGPSSNPHAKPSDFHFLKVGSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 158
 DB 85 LGPSSNPHAKPSDFHFLKVGSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 144
 QY 159 SERVLKKNVGHPLFVGLHFSFQTADKLYFVLVDYINGGELFYHLQERCFLEPRARYAA 218
 DB 145 SERVLKKNVGHPLFVGLHFSFQTADKLYFVLVDYINGGELFYHLQERCFLEPRARYAA 204
 QY 219 EIASALGYLHSLNIVYRDLKPNILLDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPPEYL 278
 DB 205 EIASALGYLHSLNIVYRDLKPNILLDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPPEYL 264
 QY 279 APEVLHKQPYDRTVDWVWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLKPNITNSA 338
 DB 265 APEVLHKQPYDRTVDWVWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLKPNITNSA 324

QY 339 RHLLEGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFNPVNSGPNDRH 398
 DB 325 RHLLEGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFNPVNSGPNDRH 384
 QY 399 FDPEFTPEPVPNSIGKSPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 445
 DB 385 FDPEFTPEPVPNSIGKSPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 431

RESULT 5
 AAW54025
 ID AAW54025 standard; Protein; 431 AA.
 AC AAW54025;
 XX 31-JUL-1998 (first entry)
 DT Human protein kinase HPK-3.
 DE
 XX Protein kinase; human; HPK; signalling cascade; kinase expression;
 KW Alzheimer's disease; cancer; anti-inflammatory agent; immunosuppressor;
 KW asthma; multiple sclerosis; rheumatoid arthritis; lymphocytic leukaemia;
 KW lymphoma; therapy.
 XX Homo sapiens.
 OS
 XX
 PN WO9811234-A2.
 XX 19-MAR-1998.
 PD
 XX 10-SEP-1997; 97WO-US15923.
 PF
 XX 12-SEP-1996; 96US-0712709.
 PR
 XX (INCY-) INCYTE PHARM INC.
 PA
 XX Au-Young J, Guegler KJ, Hawkins PR;
 PI WPI; 1998-207394/18.
 DR N-PSDB; AAV23833.
 XX
 XX New isolated human protein kinase(s) - used to develop products for
 PT diagnosis and treatment of e.g. Alzheimer's disease, cancers,
 PT asthma, multiple sclerosis or rheumatoid arthritis
 XX
 PS Claim 23; Fig 3; 75pp; English.
 XX
 XX This sequence is a human protein kinase (HPK) of the invention. The
 CC HPK protein can be used to develop products for studying signalling
 CC cascades in various cells and tissues, diagnosing disease and selecting
 CC inhibitors or drugs with the potential to intervene in various disorders
 CC or diseases in which altered kinase expression is implicated. The
 CC products can be used to e.g. reverse memory loss such as due to
 CC Alzheimer's disease, for cancer treatment or to provide anti-inflammatory
 CC and immunosuppressive effects in the treatment of e.g. asthma, multiple
 CC sclerosis, rheumatoid arthritis, as well as certain cancers, e.g.
 CC lymphocytic leukaemias or lymphomas.
 XX

Query Match 91.7%; Score 2146; DB 19; Length 431;
 Best Local Similarity 99.5%; Pred. No. 1.6e-191;
 Matches 405; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 39 LAFMKQRMGLNDFIQIANNYSACKHPEVQSILKISQOPELMNANPPSPSQOIN 98
 DB 25 LAFMKQRMGLNDFIQIANNYSACKHPEVQSILKISQOPELMNANPPSPSQOIN 84
 QY 99 LGPSSNPHAKSDPHFLKVIKSGFGKVLARHVAEYFAVKVLOKAILKKKEKHIM 158
 DB 85 LGPSSNPHAKSDPHFLKVIKSGFGKVLARHVAEYFAVKVLOKAILKKKEKHIM 144

QY 159 SERNVLLKNVQHPFLVGLHFSQTADKLYFVLDYINGBELFYHLQERCFLEPRARYAA 218
 DB 145 SERNVLLKNVQHPFLVGLHFSQTADKLYFVLDYINGBELFYHLQERCFLEPRARYAA 204
 QY 219 ETASALGYLHSLNIVYRDILKPNILLDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
 DB 205 ETASALGYLHSLNIVYRDILKPNILLDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
 QY 279 APEVLHKQPYDRTVDWMLGAVLYEMLYGLPPFYSRNTAEMVDNIINKPLQLKPNITNSA 338
 DB 265 APEVLHKQPYDRTVDWMLGAVLYEMLYGLPPFYSRNTAEMVDNIINKPLQLKPNITNSA 324
 QY 339 RHLLEGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFNPVNSGPNDRH 398
 DB 325 RHLLEGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFNPVNSGPNDRH 384
 QY 399 FDPEFTPEPVPNSIGKSPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 445
 DB 385 FDPEFTPEPVPNSIGKSPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 431

RESULT 6
 AAY95279
 ID AAY95279 standard; Protein; 431 AA.
 XX
 AC AAY95279;
 DT 12-SEP-2000 (first entry)
 XX
 DE Human serum and glucocorticoid-induced protein kinase.
 XX
 KW Serum and glucocorticoid-induced protein kinase; SGK;
 KW human; phosphorylation; cancer; diabetes; ischaemia; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 256
 FT Modified-site 422 /note= "O-phosphorylated"
 FT Modified-site 422 /note= "O-phosphorylated"
 FT
 XX WO2000035946-A1.
 PN 22-JUN-2000.
 PD
 XX 14-DEC-1999; 99WO-GB04232.
 XX 14-DEC-1998; 98US-0112217.
 PR 19-AUG-1999; 99GB-0019676.
 XX (UYDU-) UNIV DUNDEE.
 XX Cohen P, Kobayashi T, Deak M;
 XX WPI; 2000-442364/38.
 DR
 XX Modulation of serum and glucocorticoid-induced protein kinase (SGK) by
 PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1
 PT (PDK1) or dephosphorylation, useful for treatment of cancer, diabetes
 PT and ischemic diseases -
 XX Disclosure; Fig 13; 127pp; English.
 PS
 XX The present sequence is that of human serum and
 CC glucocorticoid-induced protein kinase (SGK). SGK was initially
 CC identified as a glucocorticoid and osmotic stress-responsive gene.
 CC It is activated by phosphorylation of its Thr-308 and Ser-472
 CC residues. Novel isoforms of SGK, i.e. SGK2 and SGK3 (see
 CC AAY9275-78), have been identified. The invention provides methods
 CC of activating SGK activity by phosphorylation using
 CC 3-phosphoinositide-dependent protein kinase-1 (PDK1), and of
 CC reducing the activity of SGK by dephosphorylation. The invention

CC also provides a method of identifying a compound that modulates the
 CC activity of SGK. Such compounds are useful for treating patients
 CC requiring modulation of SGK, such as patients with cancer, diabetes
 CC or ischaemic disease.

XX Sequence 431 AA;

Query Match 91.5%; Score 2141; DB 21; Length 431;
 Best Local Similarity 99.3%; Pred. No. 4.7e-191;
 Matches 404; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 39 LAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQPEPELMNANSPPPSPSQOIN 98
 :|||||
 Db 25 IAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQPEPELMNANSPPPSPSQOIN 84
 :|||||

QY 99 LGPSSNPHAKPSDFHFLKVGKSGFKVLLARHKAEEVFYAVKVLQKAILKKKEKHIM 158
 :|||||
 Db 85 LGPSSNPHAKPSDFHFLKVGKSGFKVLLARHKAEEVFYAVKVLQKAILKKKEKHIM 144
 :|||||

QY 159 SERNVLLKNVKKHPLVGLHFSFQTADKLYFVLVDYINGGELFYHLQRCERCFLEPRARFYAA 218
 :|||||
 Db 145 SERNVLLKNVKKHPLVGLHFSFQTADKLYFVLVDYINGGELFYHLQRCERCFLEPRARFYAA 204
 :|||||

QY 219 EIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
 :|||||
 Db 205 EIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
 :|||||

QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPLQLKPNITNSA 338
 :|||||
 Db 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPLQLKPNITNSA 324
 :|||||

QY 339 RHLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVSGPNDLRH 398
 :|||||
 Db 325 RHLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVSGPNDLRH 384
 :|||||

QY 399 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 445
 :|||||
 Db 385 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 431
 :|||||

RESULT 7

AAB24116
 ID AAB24116 standard; Protein; 431 AA.

XX AAB24116;

AC AAB24116;

DT 29-JAN-2001 (first entry)

XX Rat serum and glucocorticoid regulated kinase protein (RSGK).

XX Human; STK3; serine threonine kinase; HSGK; RSGK;

XX serum and glucocorticoid regulated kinase.

XX Rattus sp.

XX CN1259573-A.

XX 12-JUL-2000.

XX 29-OCT-1998; 98CN-0123822.

XX 29-OCT-1998; 98CN-0123822.

XX (UYFU-) UNIV FUDAN.

XX Yu L, Fu Q, Zhao Y;

XX WPI; 2000-587991/56.

XX New human serine threonine protein kinase, its code sequence,
 PT preparation, and use -

XX Example 3; Fig 4; 29pp; Chinese.

XX The present invention describes human serine threonine kinase STK3,
 CC which is a new member of the serine/threonine protein kinase family.
 CC Human STK3 shares homology with human serum and glucocorticoid
 CC regulated kinase (HSGK) and rat SGK (RSGK). The present sequence
 CC represents the rat RSGK protein sequence from the present invention.

XX Sequence 431 AA;

Query Match 90.5%; Score 2118; DB 21; Length 431;
 Best Local Similarity 97.3%; Pred. No. 6.6e-189;
 Matches 396; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 39 LAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQPEPELMNANSPPPSPSQOIN 98
 :|||||
 Db 25 IAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQPEPELMNANSPPPSPSQOIN 84
 :|||||

QY 99 LGPSSNPHAKPSDFHFLKVGKSGFKVLLARHKAEEVFYAVKVLQKAILKKKEKHIM 158
 :|||||
 Db 85 LGPSSNPHAKPSDFHFLKVGKSGFKVLLARHKAEEVFYAVKVLQKAILKKKEKHIM 144
 :|||||

QY 159 SERNVLLKNVKKHPLVGLHFSFQTADKLYFVLVDYINGGELFYHLQRCERCFLEPRARFYAA 218
 :|||||
 Db 145 SERNVLLKNVKKHPLVGLHFSFQTADKLYFVLVDYINGGELFYHLQRCERCFLEPRARFYAA 204
 :|||||

QY 219 EIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
 :|||||
 Db 205 EIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
 :|||||

QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPLQLKPNITNSA 338
 :|||||
 Db 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPLQLKPNITNSA 324
 :|||||

QY 339 RHLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVSGPNDLRH 398
 :|||||
 Db 325 RHLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVSGPNDLRH 384
 :|||||

QY 399 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 445
 :|||||
 Db 385 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 431
 :|||||

RESULT 8

AAY93530

ID AAY93530 standard; Protein; 431 AA.

XX AAY93530;

AC AAY93530;

DT 25-SEP-2000 (first entry)

XX A rat serum and glucocorticoid induced protein kinase.

XX Protein kinase; Pkh1; Pkh2; Ypk1; Yrk2; protein kinase B-alpha;

XX serum and glucocorticoid induced protein kinase; SGK; PKBalpha;

XX 3-phosphoinositide-dependent protein kinase-1; PKI; fungal infection;

XX thrush; cancer; diabetes; obesity; antifungal; Candida infection.

XX Rattus sp.

XX WO200036135-A2.

XX 22-JUN-2000.

XX 14-DEC-1999; 99WO-GB04228.

XX 14-DEC-1998; 98US-0112114.

XX (MEDI-) MEDICAL RES COUNCIL.

XX (REGC) UNIV CALIFORNIA.

XX Thorner JW, Alessi DR, Torrance PD, Casamayor A;

XX WPI; 2000-442391/38.

QY 377 LINKKITPPNPNVSGNDLRHFDPEETPEPNSIGKSPDSVLVTASVKEAAEAFGLGFS 436
DB 362 LINKKITPPNPNVSGPSDLRHFDPETPEPVPSSIGRSIPDSILVTASVKEAAEAFGLGFS 421
QY 437 YAPPTDSFL 445
DB 422 YAPPVDSFL 430

RESULT 10
AAAY48573
ID AAY48573 standard; Protein; 388 AA.
AC AAY48573;
XX
XX 08-DEC-1999 (first entry)
XX Human breast tumour-associated protein 34.
DE
XX Expressed sequence tag; EST; human; breast; cancer; gene therapy;
KW treatment; tumour; cytostatic; medicament.
XX
XX Homo sapiens.
XX
XX DE19813839-A1.
XX
XX 23-SEP-1999.
XX 20-MAR-1998; 98DE-1013839.
XX 20-MAR-1998; 98DE-1013839.
XX
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
XX
XX WPI; 1999-528981/45.
DR N-PSDB; AAZ33647.
XX
XX Human nucleic acid sequences and protein products from tumor breast
PT tissue, useful for breast cancer therapy -
PT
XX Claim 22; 157-158; 188pp; German.
XX
XX This invention describes novel human nucleic acid sequences from tumor
CC breast tissue which have cytostatic activity. The nucleic acid sequences
CC can be used to produce and isolate full-length gene sequences. They can
CC be used to express proteins, which can be used as tools to find an
CC activity against breast cancer. The sequences can be used in sense or
CC antisense form. They are especially useful for medicaments for gene
CC therapy to treat breast cancer. AAY48540-Y48617 represent protein
CC fragments encoded by the expressed sequence tags described in the method
CC of the invention.
XX
SQ Sequence 388 AA;

Query Match 85.1%; Score 1992; DB 20; Length 388;
Best Local Similarity 99.2%; Pred. No. 3.3e-177;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 66 PEVQSILKISQBPPELMNPNPSPSPSQOINIGPSSNPHAKPSDFHFLKVGKSGFGK 125
DB 9 PEVQSILKISQBPPELMNPNPSPSPSQOINIGPSSNPHAKPSDFHFLKVGKSGFGK 68
QY 126 VLLARHKAEEVFYAVKVLQKAILKKEEKHIMSERVLLKNVGHFVLGLHFSFQTADK 185
DB 69 VLLARHKAEEVFYAVKVLQKAILKKEEKHIMSERVLLKNVGHFVLGLHFSFQTADK 128
QY 186 LYFVLDYINGELFYHLQRCFCLEPRARFYAAETASALGYLHSLNIVYRDLKPENILLD 245
DB 129 LYFVLDYINGELFYHLQRCFCLEPRARFYAAETASALGYLHSLNIVYRDLKPENILLD 188

QY 246 SQGHIVLTDFGLCKENIEHNSTTSTFCGTPEYLAPEVLHKOPYDRTVDMWCLGAVLYEML 305
DB 189 SQGHIVLTDFGLCKENIEHNSTTSTFCGIPEYLAPEVLHKOPYDRTVDMWCLGAVLYEML 248
QY 306 YGLPPFPYSRNTAEYDNLNKLPLQKPNITNSARHLLLEGLLOKDRTKRLGAKDDFMEIKS 365
DB 249 YGLPPFPYSRNTAEYDNLNKLPLQKPNITNSARHLLLEGLLOKDRTKRLGAKDDFMEIKS 308
QY 366 HVFFSLINWDDLINKKITPPNPNVSGPNDLRHFDPEETPEPNSIGKSPDSVLVTASV 425
DB 309 HVFFSLINWDDLINKKITPPNPNVSGPNDLRHFDPEETPEPNSIGKSPDSVLVTASV 368
QY 426 KEAAEAFGLGFSYAPPTDSFL 445
DB 369 KEAAEAFGLGFSYAPPTDSFL 388

RESULT 11
AAB99815
ID AAB99815 standard; Protein; 373 AA.
XX
XX AAB99815;
XX
XX 20-SEP-2001 (first entry)
XX AGC protein kinase family member SGK protein sequence.
XX
XX Protein kinase; identification; hydrophobic pocket; interacting;
KW cancer; diabetes; inhibition; apoptosis; tissue injury;
KW ischaemic injury; stroke.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX WO200144497-A2.
XX
XX 21-JUN-2001.
XX
XX 04-DEC-2000; 2000MO-GB04598.
XX
XX 02-DEC-1999; 99US-0168559.
XX
XX (UYDU-) UNIV DUNDEE.
XX
XX Alessi D, Biondi R;
XX
XX WPI; 2001-390252/41.
XX
XX Identifying modulators of protein kinase (PK) activity, useful in
PT developing drugs for treating cancer or diabetes, by measuring the
PT ability of the compound to modulate or mimic the interaction of PK with
PT interacting polypeptides -
XX
XX Disclosure; Fig 15; 180pp; English.
XX
XX The present invention describes a method for identifying a compound that
CC modulates protein kinase activity. The method comprises measuring the
CC ability of the compound to inhibit, promote or mimic the interaction of
CC a hydrophobic pocket-containing protein kinase with an interacting
CC polypeptide. The interacting polypeptide interacts with the hydrophobic
CC pocket of the protein kinase and/or comprises the amino acid sequence
CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (I). The method is useful in screening assays
CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides
CC or polynucleotides from the present invention are useful in medicine,
CC particularly in the manufacture of a medicament for treating a patient
CC in need of modulation of signalling by a hydrophobic pocket-containing
CC protein kinase. Specifically, the patient has cancer or diabetes or is
CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue
CC injury or ischaemic injury, including stroke. The compound or
CC composition is also useful for inhibiting the degree or rate of
CC phosphorylation by the protein kinase. The interacting polypeptide or
CC compound is useful in methods of stabilising a hydrophobic pocket-
CC containing protein kinase, where the protein kinase is exposed to the

KW Alzheimer's disease; cancer.
OS Homo sapiens.
XX EP889127-A1.
XX PD 07-JAN-1999.
XX PF 18-JUN-1998; 98EP-0304830.
XX PR 23-DEC-1997; 97US-0997212.
XX PR 01-JUL-1997; 97US-0051446.
XX PA (SMIK) SMITHLINE BEECHAM CORP.
XX PI Kumar S, Zou C;
XX DR WPI; 1999-062658/06.
XX DR N-PSDB; AAV99653.
XX PT New nucleic acid encoding human H-SGK2 poly-peptide(s) - useful for
XX PT diagnosis, treatment and prevention of e.g. arthritis, infections,
XX PT cancer, Alzheimer's disease
XX PS Claim 11; Page 8; 27pp; English.
XX CC This represents a human serum glucocorticoid-regulated kinase (H-SGK2)
CC polypeptide, a novel member of the serine/threonine protein kinase
CC family. A host cell transfected or transformed with an expression system
CC comprising the H-SGK2 nucleic acid can be used for the recombinant
CC production of the protein. The H-SGK2 polypeptide is useful for treating
CC a subject who require enhanced/reduced activity or expression/inhibition
CC of the polypeptide. Recombinant H-SGK2 is used to raise antibodies; in
CC vaccines; in drug screens; and to identify soluble or membrane-bound
CC receptors. The H-SGK2 polypeptides are useful for treating inflammation
CC (rheumatoid arthritis); septicemia; autoimmune disease (inflammatory
CC bowel disease or psoriasis); transplant rejection; infection; stroke;
CC ischaemia; renal disorders; restenosis; brain injury; acquired immune
CC deficiency syndrome; metabolic and other bone diseases (osteoporosis);
CC cancer (e.g. lymphoproliferation); atherosclerosis and Alzheimer's
CC disease. The H-SGK2 nucleic acids can be used in gene therapy.
XX SQ Sequence 496 AA;
Query Match 63.3%; Score 1481; DB 20; Length 496;
Best Local Similarity 67.7%; Pred. No. 2.4e-129;
Matches 281; Conservative 52; Mismatches 68; Indels 14; Gaps 3;
Qy 41 FMKORRGLNDFIQKIANNYSACKHPEVQSILKISQPOPELMNANSPPPP----- 91
Db 86 FIKORRAGLNEFIQNLVRYPELYKHPDVRAPLQMDSPKH----QSDPSEDEDESSQKLH 141
Qy 92 SPSQOINLGPSSNPHAKPSDFHLKVGSGFGKVLARHKAEEVFYAVKVLQKAILKK 151
Db 142 STSQINILGSGNPHAKPTDFDKVLKVGSGFGKVLAKRDLQKGFYAVKVLQKIVLNR 201
Qy 152 KEEXHIMSERNLKXKHPLFVLGHLFSFQTADKLYFVLVDYINGGELFYHLQRCFLEP 211
Db 202 KEQKHIAERNVLLKNVXKHPFLVGLHYFSQTTEKLYFVLVDVNGGELFFHLQERSPEH 261
Qy 212 RARYAAEIASALGYLSNLINIVYRDLPENILLDOSQGHVLTDFGLCKENIHNSTTTF 271
Db 262 RARYAAEIASALGYLSIKIVYRDLPENILLDOSVGHVLTDFGLCKEGIAISDTTTF 321
Qy 272 CGTPEYLAPVLLHQPDRYTDVWCLGAVLYEMLYGLPPFVSRNTAEWYDNLNKPQLK 331
Db 322 CGTPEYLAPVIRKQPYDNTVDWCLGAVLYEMLYGLPPFCRDVAEMYDNLNKPQLSLR 381
Qy 332 PNITNSARHLLGLQKDRKRLGAKDDFMEIKSHVFSSLINWDDLNKKITPPENPNVS 391
Db 382 PGVSLTAWSLTEELLELEKDRQNLGAKEDFLEIQNHPPFESLSWADLVQKKIPPPFNVA 441
Qy 392 GPNDLRHDFEPTTEEPVPSIGKSPDVLVTASVKEAAEAFLGFSYAPPT--DSFL 445

Db 442 GPDIRNFDAFTETVPYSCVSSDYSIVNASVLEADDAFVGFSYAPPSDELFL 496
RESULT 14
AAV95278
ID AAY95278 standard; Protein; 429 AA.
XX AC AAY95278;
XX DT 12-SEP-2000 (first entry)
XX DE Human serum and glucocorticoid-induced protein kinase 3.
XX KW Serum and glucocorticoid-induced protein kinase 3; SGK3;
XX KW human; phosphorylation; cancer; diabetes; ischaemia; therapy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Modified-site 77 /note= "O-phosphorylated"
XX FT Modified-site 79 /note= "O-phosphorylated"
XX PN WO200035946-A1.
XX PD 22-JUN-2000.
XX PF 14-DEC-1999; 99WO-GB04232.
XX PR 14-DEC-1998; 98US-0112217.
XX PR 19-AUG-1999; 99GB-0019676.
XX PA (UYDU-) UNIV DUNDEE.
XX PI Cohen P, Kobayashi T, Deak M;
XX DR WPI; 2000-442364/38.
XX DR N-PSDB; AAA27858.
XX PT Modulation of serum and glucocorticoid-induced protein kinase (SGK) by
XX PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1
XX PT (PDK1) or dephosphorylation, useful for treatment of cancer, diabetes
XX PT and ischemic diseases -
XX PS Disclosure; Page 7; 127pp; English.
XX CC The present sequence is that of human serum and
XX CC glucocorticoid-induced protein kinase (SGK) isoform 3. SGK
XX CC (see AAY95279) was initially identified as a glucocorticoid and
XX CC osmotic stress-responsive gene. SGK3 is activated by
XX CC phosphorylation in a similar manner to SGK. The invention provides
XX CC methods of activating SGK activity by phosphorylation using
XX CC 3-phosphoinositide-dependent protein kinase-1 (PDK1), and of
XX CC reducing the activity of SGK by dephosphorylation. The invention
XX CC also provides a method of identifying a compound that modulates the
XX CC activity of SGK. Such compounds are useful for treating patients
XX CC requiring modulation of SGK, such as patients with cancer, diabetes
XX CC or ischaemic disease.
XX SQ Sequence 429 AA;
Query Match 63.1%; Score 1476; DB 21; Length 429;
Best Local Similarity 67.5%; Pred. No. 5.7e-129;
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;
Qy 41 FMKORRGLNDFIQKIANNYSACKHPEVQSILKISQPOPELMNANSPPPP----- 91
Db 19 FIKORRAGLNEFIQNLVRYPELYKHPDVRAPLQMDSPKH----QSDPSEDEDESSQKLH 74
Qy 92 SPSQOINLGPSSNPHAKPSDFHLKVGSGFGKVLARHKAEEVFYAVKVLQKAILKK 151

Db 75 STSONINLPGSNBHAQPTDFDLKVIKGSFGKVLAKRKLKDGKFAVVKVQLKIVLNR 134
Qy 152 KEEKHINSERNVLLKNVKBPLVGLHESFOTADKLYEVLDYINGGELFYHLQERCFLEP 211
Db 135 KEQKHIAERNVLLKNVKBPLVGLHESFOTTEKLYEVLDVNGGELFFHLQERSFPEH 194
Qy 212 RARFYAAEIASALGYLSHNLVVRDLKXPNILLDSDQGHIVLTDGFLCKENIEHNTSTTF 271
Db 195 RARFYAAEIASALGYLSHNLVVRDLKXPNILLDSDQGHIVLTDGFLCKEGIAISDTTTF 254
Qy 272 CGTPEYLAPEVLHKQPYDRYVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLK 331
Db 255 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYDNLHKPLSLR 314
Qy 332 PNITNSARHLEGLLQKORTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVS 391
Db 315 PGVSLTAMSLIEELLEKDRQNLGAKEDFLEIQNHPPFESLSWADLVQKXIPPPFNVA 374
Qy 392 GPDLRHFDPFTEEPVNSIGKSPDSVLVTASVKEAAEAPLGFSAAPPT-DSFL 445
Db 375 GPDDIRNFTAFTEETVPYSVCVSSDIYNASVLEADDAFVGFSYAPPSDIFL 429

RESULT 15
AAU87228
ID AAU87228 standard; Protein; 496 AA.
XX AC AAU87228;
XX DT 05-JUN-2002 (first entry)
XX DE Novel central nervous system protein #138.
XX KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX OS Homo sapiens.
XX PN W020015318-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01332.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214896.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232197.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.

PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249219.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249284.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-581633/65.

N-PSDB; ABK43558.

New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 9; SEQ ID No 746; 837pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and ankyrotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial

CC infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 63.1%; Score 1476; DB 22; Length 496;
 Best Local Similarity 67.5%; Pred. No. 7.1e-129;
 Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;

QY	41	FMKQRMGLNDFLOKANNYSACKHPEVQSILKISQPEPELMNANPSPPP-----91
DB	86	FIKQRRAGLNEFIQNLVRYPELVNHPDVRFLQMDSPKH---OSDSEDEDESSQKLH 141
QY	92	SPSQQINLGPSSNPHAKPSDFELKVIKIGSGFKVLLARHKAEEVFYAVKVLQKALKK 151
DB	142	STSQNINLGPSCNPHAKPTDFELKVIKIGSGFKVLLAKKLDGKFYAVKVLQKIVLNR 201
QY	152	KEEKHIMSERVLLKNVGHFPLVGLHFSQFADKLYFVLDYINGGELFYHLQRCFLEP 211
DB	202	KEQKHMAERNVLLKNVGHFPLVGLHVSFQTEKLYFVLDVANGGELFFHLQERSFPEH 261
QY	212	RARFYAAETASALGYLHSLNIVYRDLPENILLDSQGHIVLTFGLCKENIEHNTSTTF 271
DB	262	RARFYAAETASALGYLHSLNIVYRDLPENILLDSVGHVVLTFGLCKEGIAISDTTTF 321
QY	272	CGTPEYLAPVHLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLQK 331
DB	322	CGTPEYLAPVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEYDNLNKPQLSLR 381
QY	332	PNITNSARHLLEGGLQKDRTRKLGAKDDFMKSHVFFSLINWDDLKINKITPPFPNVS 391
DB	382	PGVSLTAWSLLEELLEKDRQNLGAKEDFLEIQNHPPFESLSWADLVQKKI PPPFNVA 441
QY	392	GPNDLRHDFEPTPEEPVNSIGKSPSVLVTASVKEAAEFLGFSYAPPT-DSPL 445
DB	442	GPDDIRNFDTAFTEETVPYSCVSDYSIVNASVLEADDAFVGFSYAPPSDELFL 496

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